



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 188562

TO: Brendan O Baggot
Location: rem/2B59/2C18
Art Unit: 1638
Friday, May 05, 2006

Case Serial Number: 10/620914

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A55
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

RUSH

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold

REMOVE
PENDING

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 18:51:48 ; Search time 1620 Seconds
(without alignments)
9938.567 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atggggctggctgacgg.....gcgcgaagaagacaactaa 1947

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1947	100.0	1947	7	US-10-620-914-44
2	645	33.1	5242	7	US-10-620-914-43
3	100.2	5.1	1252	5	US-10-118-495-1
4	100.2	5.1	1252	7	US-10-620-914-1
5	76.8	3.9	2259	8	US-10-741-849-6021
6	73	3.7	2727	7	US-10-620-914-49
7	73	3.7	3427	7	US-10-620-914-48
8	72.4	3.7	137560	8	US-10-481-112-1
9	70	3.6	1251	5	US-10-118-495-32
10	70	3.6	1251	7	US-10-620-914-32
11	69.6	3.6	1248	5	US-10-118-495-22
12	69.6	3.6	1248	7	US-10-620-914-22
13	67.8	3.5	1104	6	US-10-204-434A-12
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22	66.6	3.4	1626	7	US-10-392-041-3
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24	66.6	3.4	1626	8	US-10-392-387-3	Sequence 3, Appli
25	65	3.3	1530	6	US-10-402-842-12	Sequence 12, Appl
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30	65	3.3	6196	5	US-10-205-032-1	Sequence 1, Appli
31	64.6	3.3	2034	7	US-10-441-949-56	Sequence 56, Appl
32	64.6	3.3	2289	7	US-10-437-963-62879	Sequence 62879, A
33	64.2	3.3	2278	9	US-10-812-271-7	Sequence 7, Appli
34	64.2	3.3	2737	8	US-10-425-115-146880	Sequence 146880,
35	64.2	3.3	2807	7	US-10-425-114-33804	Sequence 33804, A
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37	63.4	3.3	2550	3	US-09-967-464-65	Sequence 65, Appl
38	63.2	3.2	1737	8	US-10-411-910A-230	Sequence 230, App
39	63	3.2	2034	7	US-10-441-949-57	Sequence 57, Appl
40	62.6	3.2	1251	5	US-10-118-495-28	Sequence 28, Appl
41	62.6	3.2	1251	7	US-10-620-914-28	Sequence 28, Appl
42	62.6	3.2	1276	7	US-10-425-114-30664	Sequence 30664, A
43	62.4	3.2	982	8	US-10-727-010-1	Sequence 1, Appli
44	62.4	3.2	1082	3	US-09-881-165-4	Sequence 4, Appli
45	62.2	3.2	1350	8	US-10-411-910A-271	Sequence 271, App

ALIGNMENTS

RESULT 1

US-10-620-914-44
; Sequence 44, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-44

Query Match 100.0%; Score 1947; DB 7; Length 1947;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1861 CGCCCACTCAGGCTACATGCGCGCTCAACATGTACAGCTCTTCTACATGCGCCGC 1920
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QY 1921 CGGAAGGCGCGCAAGAGGCACTAA 1947
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RESULT 2
US-10-620-914-43
; Sequence 43, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 5242
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-43

Query Match 33.1%; Score 645; DB 7; Length 5242;
Best Local Similarity 100.0%; Pred. No. 2.4e-162;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1105 CCCTTCCTGTGCGAAACAGCGCAAACTTCTGTGTCGAAGCGCCTCTGTACTTCCAGCAC 1164
Db 3288 CCCTTCCTGTGCGAAACAGCGCAAACTTCTGTGTCGAAGCGCCTCTGTACTTCCAGCAC 3347
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Qy 1165 GGCCTGTACTACAGGCGGCATGGCAAGCTGTGCTGGGTGCTGAGTGCCTGSCCGTG 1224
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RESULT 3
US-10-118-495-1
; Sequence 1, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-05897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-118-495-1

Query Match 5.1%; Score 100.2; DB 5; Length 1252;
Best Local Similarity 50.9%; Pred. No. 2e-16;
Matches 299; Conservative 0; Mismatches 273; Indels 15; Gaps 2;

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Qy 869 TGGAGATCAACCCCAAGACACGCTGTGCTGACCTGACTAGCGGGGCTGCAATGCCCTGA 928
Db 182 TCGCCATCCGCGCGGAGACCGGCTGTGGCCATCGCTCGGGGGGTTGCAACGTGTTT 241
Qy 929 ACCTGTGGTGCAGGGGGCGGCGAGGTGTGTTGGTGGACTGCAACCCCGCAGTCGG 988
Db 182 TCGCCATCCGCGCGGAGACCGGCTGTGGCCATCGCTCGGGGGGTTGCAACGTGTTT 241
Qy 929 ACCTGTGGTGCAGGGGGCGGCGAGGTGTGTTGGTGGACTGCAACCCCGCAGTCGG 988
Db 929 ACCTGTGGTGCAGGGGGCGGCGAGGTGTGTTGGTGGACTGCAACCCCGCAGTCGG 988
```

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Db 242 CCTATCTACAGCAGGGCGCGGCTCGATCTCTCGCGTGGATCTCTCGCCGCCCATGTGG 301
Qy 989 CGCTTCTGAGCTCAAGAAGGTGCGCATTTACAGAGCTG---GAGTTTCAGGACGTGTGGC 1045
Db 302 CGCTGGGGCGGCTGAAGCTCGCCCGCGCGGACGCTGCCGACCATGCGCCTTCTTTCG 361
Qy 1046 AGCTGTTTGGCGAGGGCGTGCACCCGCGCATTTGAGGAGCTGTACGAGAAAGTGGCGC 1105
Db 362 ATCTCTTCGTCGCGCAGACCTGCGCGCAATGCGGCCCTCTACGACCGCCACATCGCGC 421
Qy 1106 CTTTCTGTGCGAAACACAGCCACAACCTTCTGTTCCAGCGCCTCTGTACTTCCAGCAG 1165
Db 422 CCGCGCTCGACGCGCGAGCGCGCTACTTGGGAGCGCGAGCCCTTTCGCGCGCGCA 481
Qy 1166 GCCTGTACTACAGCGGGCATGGCAAGCTGTGCTGGGTGCTGCAGTGCCTGGCGG--- 1222
Db 482 TCCAGCTGTTGAGCGGGCTTCTACCGGCACGGTGCCTCGGCGGCTTATTCGCGGGG 541
Qy 1223 -----TGGTCTGAGACTGGGCAAGACCGTCAAGCGCTTCGCCAACGCGCCACAA 1273
Db 542 CCATACGCTCGCGCGGCGCGGCAACCGACCTGCGGGCTTCTCGACTGTCCGACA 601
Qy 1274 TGGAGGAGCAGCGCGCTCTGTGGACACAGCATGCTCATCTTCTGTGAAGACGGCG 1333
Db 602 TCGAGGCGCAGCGCAGCTTCTTACGCCCATATCGGGCGCTCTTCGAGGCGCCCGTGG 661
Qy 1334 CCAAGCGCTGTGCTGTGCTCAAGTTCTGAGCTGAGCTGTGCTC 1380
Db 662 TGCAGGCGCTCGCCCGACGCGCGCGGCTTCTTCGGGCTGGGATC 708

RESULT 4
US-10-620-914-1
; Sequence 1, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-620-914-1

Query Match 5.1%; Score 100.2; DB 7; Length 1252;
Best Local Similarity 50.9%; Pred. No. 2e-16;
Matches 299; Conservative 0; Mismatches 273; Indels 15; Gaps 2;

Qy 809 TCCGCGCCACTTCTGTACAGCAGTGTGTTGGAGGACCCCGAGCCGGATATGAGGTGA 868
Db 122 TCTTCCACGGCCTCGTCTATCCGAGATCTGGGAGGATCCGCGGTGGACATGCGGCC 181
Qy 869 TGGAGATCAACCCCAAGACACGCTGTGCTGACCTGACTAGCGGGGCTGCAATGCCCTGA 928
Db 182 TCGCCATCCGCGCGGAGACCGGCTGTGGCCATCGCTCGGGGGGTTGCAACGTGTTT 241
Qy 929 ACCTGTGGTGCAGGGGGCGGCGAGGTGTGTTGGTGGACTGCAACCCCGCAGTCGG 988
Db 242 CCTATCTACAGCAGGGCGCGGCTCGATCTCTGCGGTGGATCTCTCGCGGCCCATGTGG 301
Qy 989 CGCTTCTGAGCTGCAAGAAGTGGCCATTCAGCAGCTG---GAGTTTGAAGACGTGTGGC 1045
Db 302 CGCTGGGGCGGCTGAAGCTCGCGCGCGGAGCTGCGCGACCATGCGCGCTTCTTCG 361
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Qy 1046 AGCTGTTTCGGAGGGCGTGCACCCGCGCATTTGAGGAGCTGTACGAGAAGAGCTGGCGC 1105
 Db 362 ATCTCTTCGGTCGGCGAGACTGCCGCGCAATGCGCCCTCTACGACGCGCACAATCGCGC 421
 Qy 1106 CTTTCCTGTCTGCAAAACACGAGCCACAACCTTCTGGTCCAAAGCGCTCTGGTACTTCCAGCAGC 1165
 Db 422 CCGGCTCGAGCGCGGAGCGCGCTACTTGGAGGCGCGCAGCCCTTGGCGCGCGCA 481
 Qy 1166 GCCTGTACTACAGGGCGGCATGGGCAAGCTGTGTGGTGTCTGCTGAGTGCCTGGCGC--- 1222
 Db 482 TCCAGCTGTTTCAGCGGGCGCTTACCGGCACGGTGCCTCGGCGCTTCTATCGGCGCGG 541
 Qy 1223 -----TGGTGTGGAGCTGGGCAAGACCGTCAAGCGCTCGCAACGCGCCCAAA 1273
 Db 542 CCATACGCTCGCGGGCGCGGCGACCGACCTGCGGGGCTTCTCGACTGTCCCGACA 601
 Qy 1274 TGGAGGAGCAGCGCGCTGTGGGACAGCAACATGCTCATCCACTTGTGAAGAAGCGGC 1333
 Db 602 TCGAGGCGCAGCGAGCTTCTTACGCCCATATCGGGCGCTCTTCGAGGCGCGCGTGG 661
 Qy 1334 CCAAGCGCTGGTGTGGCTGTGTCTCAAGTTCTGTGAGCGCTGGTGCTC 1380
 Db 662 TGCAGGGCGCTCGCCGAGCGCGCGCGCTCTTCGGGCTGGGATC 708

US-10-741-849-6021
 ; Sequence 6021, Application US/10741849
 ; Publication No. US2005001931A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roemer, Terry
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Boone, Charles
 ; APPLICANT: Bussey, Howard
 ; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
 ; FILE REFERENCE: 10182-023-999
 ; CURRENT APPLICATION NUMBER: US/10741,849
 ; CURRENT FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/434,832
 ; PRIOR FILING DATE: 2002-12-19
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6021
 ; LENGTH: 2259
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-10-741-849-6021

Query Match 3.9%; Score 76.8; DB 8; Length 2259;
 Best Local Similarity 54.3%; Pred. No. 4.2e-10;
 Matches 178; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

Qy 212 ACCTCATCTGGGTTGACCTGGTGTGGCACTGGGGAATGTGATATGATGCTGATT 271
 Db 323 ATCTATTGGAATGATATGTTGGTGGAACTGGTTCATATGAATTCATGATGAA 382
 Qy 272 ACATCGACCT---GGCGAAGTTCAAGTCCATCTACGTGGTGCAGCTGTGCCACTGCTGT 328
 Db 383 TTAGTAAATATCTGMAAACTTTAAAGCTGTTATTGTTGGTGTGATCTTTCCCACTTTGT 442
 Qy 329 CGAGGTGGCAAGNAGGCGGAGCGCAAGGCTGGAAGATGTCCAGGTCTGGAGG 388
 Db 443 GTGAAGTGTGAAGCAAGATTTGAAGCCCAATGAATGGACAAATGTTCAATGATTAGTTG 502
 Qy 389 CCGACGCTTGCCTTTTCGCGCCCTGAGGCGCACCGCGACGCTCATCACCTTCTCCTACT 448
 Db 503 CTGATGCTGTGATTTTACTATTGATATGATGCTGATTTGATTTACTTTTCTTATT 562
 Qy 449 CGCTCAGATGATTTCCACCGTTCCAAACGTCATCGACCGAGCTTGTCTGTAACCTGCTCC 508
 Db 563 CATTGTGATGATCCCACTTTCAATGCTGCTATCGATAATGCTGTTTCTAAATTAGATA 622

Qy 509 AAGACGCGCTGGTGGGCGTTGCCGACTT 536
 Db 623 TGGAGGTATTATTGCCACTGTGGATT 650

RESULT 6
 US-10-620-914-49
 ; Sequence 49, Application US/10620914
 ; Publication No. US20040093639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph
 ; APPLICANT: Riekhof, Wayne
 ; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-07769
 ; CURRENT APPLICATION NUMBER: US/10/620,914
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 10/118,495
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 49
 ; LENGTH: 2727
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 US-10-620-914-49

Query Match 3.7%; Score 73; DB 7; Length 2727;
 Best Local Similarity 51.0%; Pred. No. 4.5e-09;
 Matches 172; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

Qy 779 ACGAGGAGCGGTGGAGCGCGCCCATGTTCCGCCCCACTTCTCTGTACACGAGTCGT 838
 Db 1448 ACGACGATCAACTCCCCAAGACACACCAGTTCAATGACGAGTACATCTACGCCCTTTACT 1507
 Qy 839 GGGAGGACCCCGAGCCGGATATGAGGTGATGGAGATCAACCCCAAGACACAGGTGCTGA 898
 Db 1508 GGGAGACTCGCGGTGCACAGAACTCCTTAACCTCGGCGCCGACGACGCTGCTCTAG 1567
 Qy 899 CCCTGACTAGCGGCGGTGCAATGCCCTGAACCTGTGTTGGTGCAGGGCGCGCCAGGTGG 958
 Db 1568 CCATCACCAGCGCGCGACAACTTCTTCTACCTGATGACAGTCCCGCTCGCGTGC 1627
 Qy 959 TGTGCTGGTACTGCAACCCCGCGCAGTCGGCTTCTTGGAGCTGAAGAAGTGGCCATTTC 1018
 Db 1628 ACGCATCGACCTTAACCCAGCCCAAAACACCTGTGTACTCAAAGTGCCTCTTTTA 1687
 Qy 1019 AGCAGCTGGAGTTTGGAGAGCTGTGGCAGCTGTTCGGAGGGCGTGCACCCGCGCAATTG 1078
 Db 1688 CGACTCTGGATTACCCCGACGTCCTGGAAGATCTTCGGGTGAGGGCAACACCCCGACTTTC 1747
 Qy 1079 AGGAGCTGTAGGAGAAGCTGGCGCCCTTCCTGTC 1115
 Db 1748 GTCACCTGCTCATCTCCAAACTCTCCCTCACCTCTC 1784

RESULT 7
 US-10-620-914-48
 ; Sequence 48, Application US/10620914
 ; Publication No. US20040093639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph
 ; APPLICANT: Riekhof, Wayne
 ; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-07769
 ; CURRENT APPLICATION NUMBER: US/10/620,914
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 10/118,495
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 48
; LENGTH: 3427
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-48

Query Match          3.7%; Score 73; DB 7; Length 3427;
Best Local Similarity 51.0%; Pred. No. 4.8e-09;
Matches 172; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 779 ACAGGAGCGGTGGAGCGCGCCATGTTCCCGCCACCTTCTGTACACGCGAGTCGT 838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1906 AGGAGATCACTCCGAGACACCCAGTTCAATGACGAGTACATCTACGCCTTTACT 1965

QY 839 GGGAGGACCCCGAGCGCGATATGGAGGTATGGAGATCAACCCCAAGGACACGGTGTGA 898
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1966 GGGAGACTCGCGGCTCGACAGAGAACTCTTAACTCGGGCCGACGAGTCGTCCTAG 2025

QY 899 CCCTGACTAGCGCGGCTGCAATGCCCTGAACCTCTGTTGAGGGGCGCGCCAGGTGG 958
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2026 CCATCACCAGCGCGCGGCGACAACTTCTTCTACCTGATGCAGAGTCCCGCTCGCGTGC 2085

QY 959 TGTGGTGGAGTGCACCCCGCGAGTCGGCGCTTCTGAGCTGAAGAAGTGGCCATTC 1018
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2086 AGCCATGACCTAAACCCAGCCCAAAACCCCTCTTGAATCAAGTCGCTCTTTTA 2145

QY 1019 AGCAGCTGGAGTTTGAGGACGTGTGGCAGCTGTTTCGGCGAGGGCGTGCACCCGCGCATTTG 1078
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2146 CGACTCTGGATTACCCCGAGGTCTGGAAGATCTTCGGTGGGGCAACACCCCGACTTTC 2205

QY 1079 AGGAGCTGACGAGAAGAGTGGCGGCTTCCTGTC 1115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2206 GCTCACTGCTATCTCCAAACTCTCCCTCACCTCTC 2242

RESULT 8
US-10-481-112-1
; Sequence 1, Application US/10481112
; Publication No.. US20040235721A1
; GENERAL INFORMATION:
; APPLICANT: WEBER, Olaf
; APPLICANT: FRIEDERICH, Sonja, Maria
; APPLICANT: SIEGLING, Angela
; APPLICANT: SCHLAPP, Tobias
; APPLICANT: MERCER, Andrew, Allan
; APPLICANT: FLEMING, Stephen, Bruce
; TITLE OF INVENTION: Recombinant proteins of Parapoxvirus ovis and pharmaceutical comp
; TITLE OF INVENTION: therefrom.
; FILE REFERENCE: Lea 35228
; CURRENT APPLICATION NUMBER: US/10/481,112
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 137560
; TYPE: DNA
; ORGANISM: Parapoxvirus ovis NZ2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(539)
; OTHER INFORMATION: ORF: L1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (781)...(449)
; OTHER INFORMATION: ORF: L2r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1933)...(1664)
; OTHER INFORMATION: ORF: L3r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3269)...(2790)
; OTHER INFORMATION: ORF: L4r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2799)...(3851)
; OTHER INFORMATION: ORF: L5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2962)...(3753)
; OTHER INFORMATION: ORF: L6
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; NAME/KEY: CDS
; LOCATION: (3784)...(3122)
; OTHER INFORMATION: ORF: L7r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4341)...(4129)
; OTHER INFORMATION: ORF: L8r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4904)...(4428)
; OTHER INFORMATION: ORF: 1ar
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6517)...(4970)
; OTHER INFORMATION: ORF: 1r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8042)...(6684)
; OTHER INFORMATION: ORF: 2r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9889)...(8070)
; OTHER INFORMATION: ORF: 3r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11195)...(10062)
; OTHER INFORMATION: ORF: 4r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11493)...(11227)
; OTHER INFORMATION: ORF: 5r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11802)...(12038)
; OTHER INFORMATION: ORF: 6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12358)...(12080)
; OTHER INFORMATION: ORF: 7r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13980)...(12364)
; OTHER INFORMATION: ORF: 8r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14826)...(14053)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15080)...(15394)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16838)...(15423)
; OTHER INFORMATION: ORF: 11r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19021)...(16847)
; OTHER INFORMATION: ORF: 12r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19704)...(19156)
; OTHER INFORMATION: ORF: 13r
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (20314)...(19736)
; OTHER INFORMATION: ORF: 14r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20401)...(22101)
; OTHER INFORMATION: ORF: 15
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22125)...(22940)
; OTHER INFORMATION: ORF: 16
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; NAME/KEY: CDS
; LOCATION: (23003)...(23866)
; OTHER INFORMATION: ORF: 17
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26908)...(23873)
; OTHER INFORMATION: ORF: 18r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26926)...(27213)
; OTHER INFORMATION: ORF: 19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27626)...(27216)
; OTHER INFORMATION: ORF: 20r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29754)...(27616)
; OTHER INFORMATION: ORF: 21r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32217)...(29800)
; OTHER INFORMATION: ORF: 22r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33380)...(32418)
; OTHER INFORMATION: ORF: 23r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33602)...(33393)
; OTHER INFORMATION: ORF: 24r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34466)...(33612)
; OTHER INFORMATION: ORF: 25r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34735)...(34502)
; OTHER INFORMATION: ORF: 26r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35905)...(34739)
; OTHER INFORMATION: ORF: 27r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37194)...(35905)
; OTHER INFORMATION: ORF: 28r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37200)...(39248)
; OTHER INFORMATION: ORF: 29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41037)...(39229)
; OTHER INFORMATION: ORF: 30r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41374)...(42066)
; OTHER INFORMATION: ORF: 31
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (42336)...(41731)
; OTHER INFORMATION: ORF: 32r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42407)...(41997)
; OTHER INFORMATION: ORF: 33r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42410)...(43765)
; OTHER INFORMATION: ORF: 34
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43770)...(43958)
; OTHER INFORMATION: ORF: 35
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43980)...(44534)
; OTHER INFORMATION: ORF: 36

Query Match 3.7%; Score 72.4; DB 8; Length 137560;
Best Local Similarity 42.9%; Pred. No. 1.5e-08;
Matches 461; Conservative 0; Mismatches 611; Indels 2; Gaps 2;

Qy 618 CGACAACATTGACATCGGCCCGCCGCGCGCTTACCTGGAGCAGAGCTTGGAGCGGT 677
Db 20613 CGAGGTCTTCGACGCCGTGCTCAAGCGCGCTTCGACGCGCTCAGCTCTTTGTGCGGC 20672
Qy 678 GTGGAGCAGAACACCCAGGTTTCGATCCCTAGTGGCGTGGTGGCGGCCCTACTA 737
Db 20673 GCTCTCGCGCACCTTCGAGGCTTCGTTGGCGCATCCGGGCTTACCGCGGACCTGCG 20732
Qy 738 CGTGTGATTGGCGCTGCCGCGTTGGCAGCGCTGCACGAGGAGCGCGTGGAGCG 797
Db 20733 GGAGCTGCTGGCGGACGCGGCTTTCATGAGTGGTGGCGCGCGCCGAGCTCGCGGA 20792
Qy 798 GCCGCCCATGTTCCCGGCCACCTTCTGTGTACACGCACTGCTGGGAGGACCCCGAGCCGGA 857
Db 20793 GGTCAATTGGCGTGAACCAACGACATCGCGCGAACCCGCTCTTCGCGGAGCGGAGCCGT 20852
Qy 858 TATGAGGTGATGAGATCAACCCCAAGGACACGGTGTGTACCTGTACTAGCGGGGGTG 917
Db 20853 GCGGAGCGGAGGCTCATTTTCGCAAGACCTTCCGCAAGACCGAGTTCCCGCGCGTCAA 20912
Qy 918 CAATGCCCTGAACCTGCTGTGTCAGGGGCGCGGCGAGTGTGCTGGTGGACTGCAACCC 977
Db 20913 GCGCTCGCGTGTGCGGTGCTGTGTGGGCTTCTCTGTGAAGAGGACTTGGCGG 20972
Qy 978 CGCGAGTCGCGGCTTCTGGAGCTGAAGAAGGTGGCCATTTCAGAGTGGAGTTTGAGGA 1037
Db 20973 CGAGTACGCGGACAAACGACCGCCAGGACCTGTTTACGCTGTGCAGAAGCGCGGGGCC 21032
Qy 1038 CGTGTGCAGCTGTTGCGGAGGCGGTGCACCGCGGCTTTCAGGAGCTGTACGAGNAGAA 1097
Db 21033 CGTGCGCCA-CAGCGCGCTCACAGAGACATCCCGGAGTACTTTCCTCCCGGAGACAGCG 21091
Qy 1098 GCTGCGCGCTTCTGTGCAAAACAGCCACAACTTCTGTGTCCTCAAGCGCTT-CTGGTACT 1156
Db 21092 CCAGCCACTGGGTCTGGCTGNAACGCGCGGTGGCGGACGCGAGAGGTGTACCGGACC 21151
Qy 1157 TCCAGCACGGCTTGTACTTACAGGGCGGCAATGGGCAAGCTGTGTGGTGTGTGAGTGCC 1216
Db 21152 GGCCCGCGCGCACGCTCTACGAGCGGTGCTCAGTACGCGTACTCAGAGGTCAAGCAGG 21211
Qy 1217 TGGCGGTGGTGTGGGACTGGGGAAGACCGTCAAGCGCTCGCCCAACGCGGCCCAATGG 1276
Db 21212 GCGCGGTGAACGCCAACACGCTCAAGCTCGTGTACCGGCTCGAGGACACCCCGACATCA 21271
Qy 1277 AGGAGCAGCGCGCTGTGTGGGACAGCAACATGCTCATCTGTTGAAGAACGGGCCCA 1336
Db 21272 AGGCTGTGCTGACGCTCATCTACGAGTGTGCGCGGACATCGTCGGCGTCTGTGGACT 21331
Qy 1337 AGCCGTGGTGTGGCTGTTGCTCAAGTTCTGTGAGCTGGTGTCTTTCAACAGGCCGTGC 1396
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Db 21332 CCGGAAACGAGAGTGGCGGAGCTACTTCGTGAGTCTGTACCGCGAGAACTTCGTGCGAGC 21391

Qy 1397 TGTGTTTCGGCGCGCGCGTCCGGGCAAGCAGTACGCGCTGATCAAGCGGAGCGCATCC 1456

Db 21392 GACGCACTTACCTTCGGAGCGCGCTTCGGGAGACGACCTCTTCGCGGTGGTCCGCGC 21451

Qy 1457 CCAATTGAGAACTACATCGCGGCACCATGAGCGGCTGGCGGAGAACTCGCAGCTGGCGA 1516

Db 21452 TCGATCCCGACTTCTTCGAGCCCGAGCGCATCCGCGAGGCGCTTCAGCGCAGACGCGCGC 21511

Qy 1517 AGCAGAACTACTTCTACTACAACTGCTTCACCGGCAAGTCTCTCGCGCAACTCCGCCA 1576

Db 21512 TCGAGAGCGCTTCAGGACATGGACCTCAACAGCGCTTCATGTGCGACCTCATCTAG 21571

Qy 1577 CTTACTCGCGAGCGCGCTTCGCCACCTCAAGAGTGGCGTGGGACAACTTGACCG 1636

Db 21572 ACTCGTGGACCCGACGTCGCGCGCGCGAGCGGCTGCACTGCGGTGCACAACG 21631

Qy 1637 TCTCCACCAACTTCTTCATGGAGGAGCTCAAGCGCGGACCTACACCAAGTGA 1690

Db 21632 AGGACTCCGACTTACTTCATCGGGAGTACACACCTACTCTTCTCAGCGAGA 21685

RESULT 9

US-10-118-495-32

Query Match 3.6%; Score 70; DB 5; Length 1251;

Best Local Similarity 52.8%; Pred. No. 2.5e-08;

Matches 151; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Publication No. US20030074688A1

GENERAL INFORMATION:

APPLICANT: Benning, Christoph

APPLICANT: Riekhof, Wayne

APPLICANT: Klug, Rouven

TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

FILE REFERENCE: MSU-06897

CURRENT APPLICATION NUMBER: US/10/118,495

PRIOR FILING DATE: 2002-04-08

PRIOR APPLICATION NUMBER: 60/283,812

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 1251

TYPE: DNA

ORGANISM: Sinorhizobium meliloti

US-10-118-495-32

Qy 806 TGTTCGCCGCCACCTTCTGTACAGCAGTCTGTGGAGGACCCCGAGCGGATATGGAGG 865

Db 116 TGTCTTTTTCGGACTCGTCTACCGCAGATCTGGGAGGACCCGATTTGTCGACATGGAAG 175

Qy 866 TGATGGAGATCAACCCCAAGGACACGGTGTGACCTGACTAGCGGGCTGCAATGCC 925

Db 176 CGATGCGAGATCCGTCGCCGACATCGGATCTGACGATCGGTTCCGGCGGCTGCAACATGC 235

Qy 926 TGAACCTCTGCTGGTGCAGGGGCGCGGAGTGGTGTGCTGGTGGACTGCAACCCCGCGCAGT 985

Db 236 TGACCTATCTCTCCGCGAGCTGCCCGAGCTGCCCGATAGACGTGGTGCATCTCAACCCCATCACA 295

Qy 986 CGGCGCTTCTGGAGCTGAAGAGTGGCCATTAGCAGCTGGAGTTTGAGGACGTTGGC 1045

Db 296 TCGGCTCAACCGGCTGAAGCTGTCTGCTTTTCGCCACCTGCCGAGCCACAAGGACGTGG 355

Qy 1046 AGCTGTTTCGGCGAGGCGTGCACCCGCGCATTTGAGGAGCTGTACGA 1091

Db 356 TCGGTTCTCTCGCGCTCGAAGGTACGCGCAGAAATGGCCAGGCTTA 401

US-10-118-495-32

Query Match 3.6%; Score 70; DB 5; Length 1251;

Best Local Similarity 52.8%; Pred. No. 2.5e-08;

Matches 151; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Publication No. US20030074688A1

GENERAL INFORMATION:

APPLICANT: Benning, Christoph

APPLICANT: Riekhof, Wayne

APPLICANT: Klug, Rouven

TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

FILE REFERENCE: MSU-06897

CURRENT APPLICATION NUMBER: US/10/118,495

PRIOR FILING DATE: 2002-04-08

PRIOR APPLICATION NUMBER: 60/283,812

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 1251

TYPE: DNA

ORGANISM: Sinorhizobium meliloti

US-10-118-495-32

Qy 806 TGTTCGCCGCCACCTTCTGTACAGCAGTCTGTGGAGGACCCCGAGCGGATATGGAGG 865

Db 116 TGTCTTTTTCGGACTCGTCTACCGCAGATCTGGGAGGACCCGATTTGTCGACATGGAAG 175

Qy 866 TGATGGAGATCAACCCCAAGGACACGGTGTGACCTGACTAGCGGGCTGCAATGCC 925

Db 176 CGATGCGAGATCCGTCGCCGACATCGGATCTGACGATCGGTTCCGGCGGCTGCAACATGC 235

Qy 926 TGAACCTCTGCTGGTGCAGGGGCGCGGAGTGGTGTGCTGGTGGACTGCAACCCCGCGCAGT 985

Db 236 TGACCTATCTCTCCGCGAGCTGCCCGATAGAGTGGTGCATCTCAACCCCATCACA 295

Qy 986 CGGCGCTTCTGGAGCTGAAGAGTGGCCATTAGCAGCTGGAGTTTGAGGACGTTGGC 1045

Db 296 TCGGCTCAACCGGCTGAAGCTGTCTGCTTTTCGCCACCTGCCGAGCCACAAGGACGTGG 355

Qy 1046 AGCTGTTTCGGCGAGGCGTGCACCCGCGCATTTGAGGAGCTGTACGA 1091

Db 356 TCGGTTCTCTCGCGCTCGAAGGTACGCGCAGAAATGGCCAGGCTTA 401

US-10-118-495-32

Query Match 3.6%; Score 69.6; DB 5; Length 1248;

Best Local Similarity 45.0%; Pred. No. 3.1e-08;

Matches 500; Conservative 0; Mismatches 579; Indels 33; Gaps 5;

Publication No. US20040093639A1

GENERAL INFORMATION:

APPLICANT: Benning, Christoph

APPLICANT: Riekhof, Wayne

APPLICANT: Klug, Rouven

TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

FILE REFERENCE: MSU-07769

CURRENT APPLICATION NUMBER: US/10/620,914

PRIOR FILING DATE: 2003-07-16

PRIOR APPLICATION NUMBER: 10/118,495

PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.2

SEQ ID NO 32

LENGTH: 1251

TYPE: DNA

ORGANISM: Sinorhizobium meliloti

US-10-620-914-32

Qy 806 TGTTCGCCGCCACCTTCTGTACAGCAGTCTGTGGAGGACCCCGAGCGGATATGGAGG 865

Db 116 TGTCTTTTTCGGACTCGTCTACCGCAGATCTGGGAGGACCCGATTTGTCGACATGGAAG 175

Qy 866 TGATGGAGATCAACCCCAAGGACACGGTGTGACCTGACTAGCGGGCTGCAATGCC 925

Db 176 CGATGCGAGATCCGTCGCCGACATCGGATCTGACGATCGGTTCCGGCGGCTGCAACATGC 235

Qy 926 TGAACCTCTGCTGGTGCAGGGGCGCGGAGTGGTGTGCTGGTGGACTGCAACCCCGCGCAGT 985

Db 236 TGACCTATCTCTCCGCGAGCTGCCCGATAGAGTGGTGCATCTCAACCCCATCACA 295

Qy 986 CGGCGCTTCTGGAGCTGAAGAGTGGCCATTAGCAGCTGGAGTTTGAGGACGTTGGC 1045

Db 296 TCGGCTCAACCGGCTGAAGCTGTCTGCTTTTCGCCACCTGCCGAGCCACAAGGACGTGG 355

Qy 1046 AGCTGTTTCGGCGAGGCGTGCACCCGCGCATTTGAGGAGCTGTACGA 1091

Db 356 TCGGTTCTCTCGCGCTCGAAGGTACGCGCAGAAATGGCCAGGCTTA 401

US-10-118-495-22

Query Match 3.6%; Score 69.6; DB 5; Length 1248;

Best Local Similarity 45.0%; Pred. No. 3.1e-08;

Matches 500; Conservative 0; Mismatches 579; Indels 33; Gaps 5;

Publication No. US20030074688A1

GENERAL INFORMATION:

APPLICANT: Benning, Christoph

APPLICANT: Riekhof, Wayne

APPLICANT: Klug, Rouven

TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

FILE REFERENCE: MSU-06897

CURRENT APPLICATION NUMBER: US/10/118,495

PRIOR FILING DATE: 2002-04-08

PRIOR APPLICATION NUMBER: 60/283,812

PRIOR FILING DATE: 2001-04-13

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.1

SEQ ID NO 22

LENGTH: 1248

TYPE: DNA

ORGANISM: Mesorhizobium loti

US-10-118-495-22

Qy 704 TCCCTACGTGCGCTGGCTGGCGCCCTTACTACGTGTGATTTGGCGGCTGCCACG 763

Db 11 TCTCTCGGATCTGTTTTCGCGCGGCAAGGAAGTTGGAAGGCGCTCTACCAGAAC 70

RESULT 10

US-10-620-914-32

Sequence 32, Application US/10620914

Db 653 AGCTTTTGAATGGGGACCTCGCGTAAGGCTCTGCTGTTGCGCTCGCAATCCGCGG 712

Qy 1421 GCAACAGTACGCGTGTATCAAGGGCGGACGGCATCCCATTTAGAACTACATCGCGCGCA 1480

Db 713 CGCAGTACGATTCCCTGTATCACTCAGGCGACGGCACCATGSCCAGCGTTCTGAAGGCC 772

Qy 1481 CCATGGAGGGGTGGGGAGAACTCGCAGTGGCGGCAAGCAGAACTACTTCTACTACAAT 1540

Db 773 GGCTGGAAGAAGTCGCCCTGCGATTTTCCTCCCTGGAAAAAACAATTATTTCCGCTTGGCAGGTT 832

Qy 1541 GCCTCACCGGCAAGTTCCTGCGCGCAAACTGC-----CCCACTTACCTGCGCGAGGGCG 1594

Db 833 TTGCGCGCGGTATCCAAATCCGCTGAGGCGCGCCCTGCGCCCTATCTGGAAGAAGCAGA 892

Qy 1595 CTTTCCGCCACCCCT-----CAAGAGTGGGTGGTGGCAAACTGACCGTCTTCCACCAACT 1648

Db 893 ACTACGAAACCATCCGCGGCAATATCGACCGGTGCGCCATCCACCATGCAATCTGATCG 952

Qy 1649 TCTTATGAGGAGTCAAGGGCGCACCTACCAAGGTGATTTCTGATGGACACGTTGG 1708

Db 953 AATTCTCGCGGCAAGGACGCGGACCGGTGCGATCGCTTTCATCTGCTGATGCGCAGG 1012

Qy 1709 ACTGCTCGATATGCCGTGGCCAAAGAGCTGGCGAGTGCCTGGCCAAAGCAGGTTGGC 1768

Db 1013 ACTGATGACCGATGACAGCTCAACGGCTGTGTGCGAAATCAGCGCGCGCTCCG 1072

Qy 1769 CGGCGCGCATCGTATCTGGCGCTCCGCTCC 1800

Db 1073 CAGGCGCGCGTCTATCTTCGCGACCGCGCC 1104

RESULT 13

US-10-204-434A-12

; Sequence 12, Application US/10204434A

; Publication No. US20030170662A1

; GENERAL INFORMATION:

; APPLICANT: SETO, Haruo

; APPLICANT: KUZUYAMA, Tomohisa

; TITLE OF INVENTION: A Method For Screening A Substance Which Specifically Inhibits No

; TITLE OF INVENTION: Mevalonate Pathway

; FILE REFERENCE: P22747

; CURRENT APPLICATION NUMBER: US/10/204,434A

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: PCT/JP01/01501

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 1104

; TYPE: DNA

; ORGANISM: Streptomyces sp.

US-10-204-434A-12

Query Match 3.5%; Score 67.8; DB 6; Length 1104;

Best Local Similarity 45.1%; Pred. No. 9.3e-08;

Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

Qy 1344 GGTGTGGCTGTTCTGTCGAAGTTCTGTGAGCTGTGCTCTTCAACAGGCGGTGCTGTGGTT 1403

Db 513 GGTCCCGCAGATCGAAGAAGATCGGCGCGGTGACATCCCGTGTATCGTCAAGGAGGT 572

Qy 1404 CGGCGGCGGTGCGGGCAAGCAGTACGCGTGTGCTCTTCAACAGGCGGTGCTGTGGTT 1463

Db 573 CGGCAACGGCTTGAGCGCGCAGACCATCTGCTGCTCCGACCTCGCGGTGCGAGGCGC 632

Qy 1464 GAACTACATCGCGGCACATGAGCGGTGGCGAGAACTCGACGTCGCGCAGCAGAA 1523

Db 633 GGAGTCAGCGCGCGCGCGCAGCGACTTCGCGCGCATCAGAAACGCGCCCGGAGCT 692

Qy 1524 CTACTTCTACTAGAACTGCCTCACCGGCAAGTTCTGCGCGCAGAACTGCCCCACCTACT 1583

Db 693 CGGCGACTACGGTTCTTGACAGGCTGGGGGAGTTCACACCGCGCTGCTGCTGGAGCG 752

Qy 1584 CGCGAGCGCGCTTCGCCACCCCTCAAGAGTGGCGTGGTGAACAACCTGACCGTCTCCAC 1643

Db 753 CCAGGACATCTCCCTGCGCGCTCCTCGCTCGCGCGGTGTGCGTCAACCGCTCGACGTGGT 812

Qy 1644 CAATTTTTCATGAGGAGCTCAAAAGCGCGCACCTACACCAAGGTGATTTCTGATGGACCA 1703

Db 813 CGGCGCTTCCGCGTTCGCGCGCGCGCGTGGCTCTCTCCGCGCGGTCTCTTGGCAGCCCT 872

Qy 1704 CGTGGACTGGTGGATATGCCCGTGGCCCAACAGCTGGCTGCGCTGGCCCAAGCAGGT 1763

Db 873 GATGGACGACGCGCTCGACGCGCTGATCAAGAGCTCACGACCTGGCTGGACCGAGCTGGC 932

Qy 1764 TGGCGGGCGGCGATCGTATCTGGCGCTCGCGCTCCCTCAGCGCGCCCTAGCGCGAGCT 1823

Db 933 GGCCTGCGACCATGTCTGCGCGCGCGCACCCCGCGCGACCTCACCGCTGCGAGTGTCT 992

Qy 1824 GATCCAGAAGCGCGCTTCGACGTGCGTGTATCCGCGCGCGCACTCAGGGGTATACATGA 1883

Db 993 GCTCCACGGCGAGCTGGTGACTTCTGGCGCGACGCGGGGATCGACACGCGCGCTCGC 1052

Qy 1884 CCGGCTCAACATGTACAGC 1902

Db 1053 CCAGCGCTCCAGCTCCATC 1071

RESULT 14

US-09-918-740-57

; Sequence 57, Application US/09918740

; Publication No. US20030033626A1

; GENERAL INFORMATION:

; APPLICANT: Hahn, Frederick

; APPLICANT: Kuehnle, Adelheid

; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways t

; TITLE OF INVENTION: create novel traits in transgenic organisms

; FILE REFERENCE: KAS-103XCI

; CURRENT APPLICATION NUMBER: US/09/918,740

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: 60/221,703

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 57

; LENGTH: 6798

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Streptomyces sp Cll190 gene cluster containing mevalonate pathway

; OTHER INFORMATION: and lpp isomerase orfs

US-09-918-740-57

Query Match 3.5%; Score 67.8; DB 3; Length 6798;

Best Local Similarity 45.1%; Pred. No. 1.4e-07;

Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

Qy 1344 GGTGTGGCTGTTCTGTCGAAGTTCTGTGAGCTGTGCTCTTCAACAGGCGGTGCTGTGGTT 1403

Db 3835 GGTCCCGCAGATCGAAGAATCGCGCGCGGTGCGATCCCGTGTATCGTCAAGGAGGT 3894

Qy 1404 CGGCGGCGGTGCGGGCAAGCAGTACGCGCTCATCAAGCGGACGCGCATCCCATTTGA 1463

Db 3895 CGGCAACGGCTTGAGCGCGCGCAGACCATCTGCTGCTGCCGACCTCGCGGTGCGAGGCGC 3954

Qy 1464 GAACTACATCGCGGCACCATGGACGGGTGGCGAGAACTCGACGTCGCGCAGCAGAA 1523

Db 3955 GGAGCTCAGCGCGCGCGCGCGCAGGACTTCGCCCGCATCGAGAAGCGCGCGCGGAGCT 4014

Qy 1524 CTACTTCTACTAACAATGCTCTCACGGGAGTTCTTGGCGGACAACTGCCCCCAGCTTACCT 1583

Db 4015 CGGCGACTACGCGTTCTTGCACGCGTGGGGGAGTTCACACCGCGCTGCTGCTGGAGCG 4074

Qy 1584 CGCGAGGCGCGCTTCGCCACCCCTCAAGAGTGGGTGGTGGACAACTGACCGCTCTCCAC 1643

Db 4075 CCAGGACATCTCCCTGCCCGTCTCGCGTCCGCGGCGGTGTGCGTCAACCGCTCGAGCTGGT 4134

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QY 1644 CAACTTCTTCATGAGGAGCTCAAGCGCGCACCTACACCAAGTGATTCTTGATGGACCA 1703
Db 4135 CCGCGCCCTCGCGTCTCGCGCGCCGCGTCCGCTCCCTCCCGCGCTTCCTTGGCACCCCT 4194
QY 1704 CGTGACTGGCTGGATATGCCGCTGGCCCAACGAGCTGGCGGAGTGCCCTGGGCCAAGCAGGT 1763
Db 4195 GATGGACACCGGCTGCGACGCGCTGATCAGCAAGCTCAGACCTGGCTGGACCAAGCTGGC 4254
QY 1764 TCGCGCGCGCGGCATCGTCAATCTGGCGTTCGCGCTCCCTCAGCCGCGCCCTTACGCGGAGCT 1823
Db 4255 GCGCGTGCAGACCATGCTCGCGCGCGCACCCCGCGCCGACCTCACCCGCTGCGACGTGCT 4314
QY 1824 GATCCAGAAGCGGGCTTCGACGCTGCGCTGCATCGCGCGCGCCACTCAGGGCTACATGGA 1883
Db 4315 GCTCCACGGCGAGCTGCGTGACTTCTGCGCGCACCGGGGCATCGACACGCGCGCTCGC 4374
QY 1884 CCGCGTCAACATGTACAGC 1902
Db 4375 CCAGCGCTCCAGCTCCATC 4393

RESULT 15
US-10-204-434A-13
; Sequence 13, Application US/10204434A
; Publication No. US20030170662A1
; GENERAL INFORMATION:
; APPLICANT: SETO, Haruo
; APPLICANT: KUZUYAMA, Tomohisa
; TITLE OF INVENTION: A Method For Screening A Substance Which Specifically Inhibits No
; TITLE OF INVENTION: Mevalonate Pathway
; FILE REFERENCE: P22747
; CURRENT APPLICATION NUMBER: US/10/204,434A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP01/01501
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 6798
; TYPE: DNA
; ORGANISM: Streptomyces sp.
US-10-204-434A-13

Query Match 3.5%; Score 67.8; DB 6; Length 6798;
Best Local Similarity 45.1%; Pred. No. 1.4e-07;
Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

QY 1344 GGTGTGGCTGTTCGTCFAAGTTTCGTGAGCCTGGTGTCTTCAACAAGGCCGTGTGTGGTT 1403
Db 3835 GGTCCCGCAGATCGAAGAAGATCGCGCGCGCTCGACATCCCGTGATCGTCAAGGAGGT 3894
QY 1404 CGCGCGCGCGTGGCGGCAAGCAGTACGCGCTGATCAAGCGCGACCGCATCCCCATTGA 1463
Db 3895 CGGCAACGGCTGAGCCGGCAGACCATCTGCTGCTCGCGACCTCGGCGTGCAGGCGGC 3954
QY 1464 GAACATACATCGCGCGCACCATGGACGGCGTGGCGGAGAACTCGCACGTGGCGCAAGCAAA 1523
Db 3955 GGACGTACAGCGCGCGCGCGCACCGGACTTCGCCCGCATCAGAAACGGCCCGCGGAGCT 4014
QY 1524 CTACTTCTACTACAACTGCCTCACCGGCAAGTTCTCGCGGACAACTGCCCCACCTACCT 1583
Db 4015 CGGCACTACGGGTTCTCGACGGCTGGGGGAGTCCACCGCGCGCTGCTGTGGACGC 4074
QY 1584 CGCGGAGCGCGCTTCGCCACCTCAAGAGTGGGTGGTGACAACTGACCGCTTCCAC 1643
Db 4075 CCAGGACATCTCCCTGCGCGCTCTCGCTCGCGCGGTGTGGTCAACCGCTCGACGTGGT 4134
QY 1644 CAACTTCTTCATGAGGAGCTCAAGCGCGCACCTACACCAAGTGATTCTTGATGGACCA 1703
Db 4135 CCGCGCCCTCGCGTCTCGCGCGCCGCGTCCGCTCCCTCCCGCGCTTCCTTGGCACCCCT 4194
QY 1704 CGTGACTGGCTGGATATGCCGCTGGCCCAACGAGCTGGCGGAGTGCCCTGGGCCAAGCAGGT 1763
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Db 4195 GATGGACACGCGCTTCGACGCGCTGATCAGCAAGCTCAGACCTGGCTGGACCAAGCTGGC 4254
QY 1764 TCGCGCGCGCGGCATCGTCAATCTGGCGTTCGCGCTCCCTCAGCCGCGCCCTTACGCGGAGCT 1823
Db 4255 GCGCGTGCAGACCATGCTCGCGCGCGCACCCCGCGCCGACCTCACCCGCTGCGACGTGCT 4314
QY 1824 GATCCAGAAGCGGGCTTCGACGCTGCGCTGCATCGCGCGCGCCACTCAGGGCTACATGGA 1883
Db 4315 GCTCCACGGCGAGCTGCGTGACTTCTGCGCGCACCGGGGCATCGACACGCGCGCTCGC 4374
QY 1884 CCGCGTCAACATGTACAGC 1902
Db 4375 CCAGCGCTCCAGCTCCATC 4393

Search completed: May 4, 2006, 19:49:06
Job time : 1624 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 18:09:12 ; Search time 363 Seconds
(without alignments)
9534.194 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atggggctggctgacgg.....gcgccaaaggagacaactaa 1947

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCRTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.4	3.6	3003	3	US-09-252-991A-14790
2	69.4	3.6	3132	3	US-09-252-991A-14540
3	69.4	3.6	3411	3	US-09-252-991A-14823
4	68.2	3.5	2830	2	US-09-010-928B-1
5	63	3.2	1691	3	US-09-902-540-6564
6	63	3.2	2034	3	US-09-902-540-8514
7	63	3.2	2730	3	US-09-902-540-489
8	63	3.2	6855	3	US-09-902-540-897
9	62.4	3.2	1082	3	US-09-881-165-4
10	62.4	3.2	1167	3	US-09-902-540-2993
11	62.4	3.2	1250	3	US-09-902-540-362
12	62.2	3.2	3579	3	US-09-902-540-7318
13	62.2	3.2	5656	3	US-09-902-540-694
14	61.8	3.2	981	3	US-09-902-540-6237
15	61.8	3.2	13332	3	US-09-902-540-1047
16	61.8	3.2	19726	3	US-09-902-540-1164
17	61.6	3.2	1852	3	US-09-965-852-4
18	61.4	3.2	1281	3	US-09-902-540-7495
19	61.4	3.2	6269	3	US-09-902-540-726
20	60.8	3.1	951	3	US-09-252-991A-10513
21	60.8	3.1	1653	3	US-09-252-991A-10546
22	60.8	3.1	1701	3	US-09-252-991A-10316
23	60.4	3.1	1515	3	US-09-902-540-9184
24	60.4	3.1	9556	3	US-09-902-540-982

c	25	60.2	3.1	1563	3	US-09-902-540-8878	Sequence 8878, Ap
	26	60.2	3.1	10528	3	US-09-902-540-945	Sequence 945, App
	27	60	3.1	9818	3	US-09-902-540-987	Sequence 987, App
	28	59.6	3.1	1941	3	US-09-902-540-6922	Sequence 6922, Ap
	29	59.6	3.1	4359	3	US-09-902-540-594	Sequence 594, App
	30	59.2	3.0	1773	3	US-09-902-540-7746	Sequence 7746, Ap
	31	59.2	3.0	4854	3	US-09-902-540-768	Sequence 768, App
	32	58.8	3.0	1293	3	US-09-902-540-6161	Sequence 6161, Ap
c	33	58.8	3.0	1675	3	US-09-902-540-302	Sequence 302, App
c	34	58.4	3.0	1011	3	US-09-252-991A-12311	Sequence 12311, A
	35	58.4	3.0	1236	2	US-08-440-856A-1	Sequence 1, Appli
	36	57.8	3.0	1526	3	US-09-902-540-5594	Sequence 5594, Ap
c	37	57.8	3.0	41927	3	US-09-902-540-1268	Sequence 1268, Ap
	38	57.6	3.0	4345	3	US-09-949-016-2755	Sequence 2755, Ap
	39	57.6	3.0	8346	3	US-09-949-016-14497	Sequence 14497, A
	40	57.4	2.9	975	3	US-09-365-150-3	Sequence 3, Appli
	41	57.4	2.9	2261	3	US-09-158-767-1	Sequence 1, Appli
	42	57.4	2.9	2261	3	US-09-713-794-1	Sequence 1, Appli
c	43	57.4	2.9	9191	3	US-09-902-540-918	Sequence 918, App
	44	57	2.9	1059	3	US-09-252-991A-7911	Sequence 7911, Ap
	45	57	2.9	1338	3	US-09-252-991A-7764	Sequence 7764, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-14790
; Sequence 14790, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14790
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14790

Query Match		3.6%	Score 69.4;	DB 3;	Length 3003;
Best Local Similarity		43.8%	Pred. No. 0.00015;		
Matches 454;		Conservative 0;	Mismatches 571;	Indels 12;	Gaps 3;
Qy	521	TGGCGGTTGCGGACTTCTAGCTGAGCGGCAAGTACGACCTGCCCTTGGCCGAGATGCCCT	580		
Db	1965	TGGCGGTTGAGCGGAGCAACCCGACCTCAACACGGCGGCTGCTGATCACTCAAGC	2024		
Qy	581	GGTCGCGCCGCTTCTTCTGCGCATCGATCTTCGACATCGAACATTCGACATCGCCCGC	640		
Db	2025	CGCACGGAGCGGCGAGCTCACGCCAGGAGTATCCAGCGCTGCAGCCGCACTCG	2084		
Qy	641	AGCCCGCGGCTTACCTGGAGCAGAGCTGAGCGCGTGTGGGAGCAGACACCCAGGTT	700		
Db	2085	ACCACTTCCCGGGATCAAGCTGTACATGACGCGGTCGAGCGGCTGACCATCGAGGACC	2144		
Qy	701	CGATCCCTACGTCGCGTGGCTGCGCCCTACTACTAGTGTGGATTCGCGCTGCCCA	760		
Db	2145	GGGTGCGCCCGCACCCAGTACAGTTACCTTTCGAGGAGCGCGGACCGGACGTGTTCGCG	2204		
Qy	761	CGGTTGGCCACGCCCTTCACGAGGAGCGGCTGGAGCGGCGCCCATGTTCCCGCCCACT	820		
Db	2205	AGTGGGTGCGGAGCTGGTGGCGGCTGCGAGGAGTTGCGCGAGCTGCGCCAGCTCGCCA	2264		
Qy	821	TCCTGTACACGCACTGCTGGAGGAGACCCCGAGCGGATATGGAGGTGATGGAGATCAACC	880		

Qy 1538 ACTGCCTCACGGCAAG 1554
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Db 2810 AGCGAACGAAGGCAAG 2826
| | | | |

RESULT 3
US-09-252-991A-14823/c
; Sequence 14823, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14823
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14823

Query Match 3.6%; Score 69.4; DB 3; Length 3411;
Best Local Similarity 43.8%; Pred. No. 0.00015;
Matches 454; Conservative 0; Mismatches 571; Indels 12; Gaps 3;

Qy 521 TGGCGGTTCGCGATTTCTTCTGCGGATCGATCTTCACATCGACAATTGATCATCGGCCCG 640
Db 1349 TCGCGGTTCGACGCGCAGCAACCCGACCCTCAACACCGCGCGCTGCTGATCAACTCAAGC 1290
Qy 581 GGTTCGCGCGTTCCTTCTGCGGATCGATCTTCACATCGACAATTGATCATCGGCCCG 640
Db 1289 CGCACAGCAGCGCGAGCTGCTCAGCCAGCGAAATGATCCAGCGCTTCGACGCCGAATCTCG 1230
Qy 641 AGTCCGCGCTTACCTTGAGCAGAAGCTGAGCGCGCTGTGGGAGCAGAAACACCCAGGGTT 700
Db 1229 ACACTGCCCCGGATCAAGCTGTATCATGACGCGGTGAGGACTGACCATCGAGAAC 1170
Qy 701 CGATCCCTTACGTGCGGTGCTCGCGCCCCTTACTACGTGTGGATTGCGCGCTGCCCA 760
Db 1169 GGCTCGCGCCGACCCAGTACAGTTCACTTGCAGACGCGCAGCCGACGTGCTCGCG 1110
Qy 761 CGCTTGCCACGCCCTTCGACGAGGCGGTGAGCGCGCGCCCATGTTCCGCGCCACT 820
Db 1109 AGTGGGTGCGCAAGCTGCTGGCGCGCTGCAGGAGTTGCGCGAGCTCGCGCAGCTCGCCA 1050
Qy 821 TCCTGTACACGCAAGTCTGTGGGAGACCCCGAGCCGGATATGGAGGTATGGAGATCAACC 880
Db 1049 GCAGCTGGCAGGACAAGGGCTTCAGGCTTACTGAACATCGACCGCG-----ACACCG 996
Qy 881 CCAAGGACACGCTGTGTAACCTGACTAGCGCGCGCTGCAATGCGCTGAACCTGCTGGTC 940
Db 995 CCTCGCGCTTCGCGGTGAAGCTCTCCGACATCGACAGCTGCTTACAAAGCCTTCGGCC 936
Qy 941 AGGGGGCGCGCAGGTGTGTGCGTGGACTGCAACCCCGCGCAGTGGCGGCTTCTGAGAC 1000
Db 935 AGCGGCTGATCTCGACCATCTTCAACCGACCCACCGCTACCGCGGTGCTGGAGGTGG 876
Qy 1001 TGAAGAGGTGGCCATTACGACGCTGAGTTTTGAGGACGTGTGGAGCTGTTTCGCGAGG 1060
Db 875 CGCGCGATTTCAGCTCGGCCCGCAGGCCCTTGAGCAGCTTACGTGCGCTCCAGCGAGC 816
Qy 1061 GCGTGCACCCCGCATTTGAGGAGCTGTACAGAGAAGAGCTGGCGCCCTTCTCTGTGCAAAA 1120
Db 815 GCACCCAGGTGCGCCTGTGAGCTTCGCGAAGGTGGAGGCGGCATACCTGCTGGCGA 756
Qy 1121 CCAGCCACAATCTTCTGCTCCAGCGCTCTGTGTAATTCAGCAACCGCGCTGTACTACAGG 1180

755	TCAACCATATCGCCCAAGTTCTTCCTCGGCGAGACCTGCTGCTTCAACCTGGCCCAAGGGTT	699
1181	CGCGCATGGGCAAGCTGTGCTGGGTGCTGAGAGTGCCTGGCCGCTGGTGGGACTGGGCA	1240
698	ACTCCCTGGGCGAGGCGGTTCGAGGCGATCCGTGGCGCTCGAGGCCAGCCTGGAGCTGCCGC	639
1241	AGACCGTCAAGCGCTTCGGCAACGCCGCCACAAATGAGAGAGCAGCGCGTCTGTGGGACA	1300
638	TGAGCATGCAAGGCGAGCTTCCTCGCGCGCGCGCGCTTTCGAGGGCTCGCTGTTCGAACA	579
1301	GCAACATGCTCATCC--ACTTCTGTCGAAGACGGGCCCCAAGCCGCTGGTGTGCTGTCTG	1357
578	CGCTGCTGCTGATCTTCGCGCTCGGTGGTGAACATGATACATCGTCTCGGCGATCCTCTACG	519
1358	TCAAGTTCGTGAGCCTGGTGTCTCTTCAACAAGGCCCGTGTGTGGTTTCGGCGCGCGGTGC	1417
518	AGAGCTTCATCCATCCGCTGACCATCTCTCGACCTCGCCCTCGGCGCGGGTTCGGCGCGC	459
1418	CGGGCAAGCAGTACGCGCTGATCAAGCGGAGCGGCATCCCCATTGAGAACTACATCGCGC	1477
458	TGCTGCGCTGATGCTGTGGCGGGCGAGAGATCGGCATCGTGGCGATCATCGGCATCATCC	399
1478	GCACCATGACGCGCTGGCGGGAGAACTCCACAGTGGCGAAGCAGAACTACTTCTACTACA	1537
398	TGCTGATCGGATGCTCAAGAAGACCGCATCATGATGATCGACTTCGCCCTCGACGCCG	339
1538	ACTGCCTCACCGGCAAG 1554	
338	AGCGCAACGAGGCAAG 322	
RESULT 4		
US-09-010-928B-1		
; Sequence 1, Application US/09010928B		
; Patent No. 5994099		
; GENERAL INFORMATION:		
; APPLICANT: Lewis, Randolph V		
; APPLICANT: Hayashi, Cheryl Y		
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA		
; TITLE OF INVENTION: CODING THEREFOR		
; NUMBER OF SEQUENCES: 29		
; CORRESPONDENCE ADDRESS:		
; ADDRESSES: BIRCH, STEWART, KOLASCH & BIRCH		
; STREET: 8110 GATEHOUSE RD. SUITE 500E		
; CITY: FALLS CHURCH		
; STATE: VIRGINIA		
; COUNTRY: UNITED STATES OF AMERICA		
; ZIP: 22042		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: PatentIn Release #1.0, Version #1.30		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/09/010,928B		
; FILING DATE: 22-JAN-1998		
; CLASSIFICATION: 435		
; ATTORNEY/AGENT INFORMATION:		
; NAME: Murphy Jr., Gerald M		
; REGISTRATION NUMBER: 28977		
; REFERENCE/DOCKET NUMBER: 1447-109P		
; INFORMATION FOR SEQ ID NO: 1:		
; SEQUENCE CHARACTERISTICS:		
; LENGTH: 2830 base pairs		
; TYPE: nucleic acid		
; STRANDEDNESS: not relevant		
; TOPOLOGY: linear		
; MOLECULE TYPE: cDNA		
; HYPOTHETICAL: NO		
; FEATURE:		
; NAME/KEY: -		
; LOCATION: 1..2830		
; OTHER INFORMATION: /note= "Flagelliform DNA sequence"		

OTHER INFORMATION: taken from the 5' region. The putative start codon is at
OTHER INFORMATION: position 219"

FEATURE:
; NAME/KEY: CDS
; LOCATION: 219..2830
US-09-010-928B-1

```
Query Match          3.5%; Score 68.2; DB 2; Length 2830;
Best Local Similarity 46.4%; Pred. No. 0.00025;
Matches 290; Conservative 0; Mismatches 333; Indels 2; Gaps 2;

Qy 772 GCCCTTGACACGAGGCGGTGGAGCGCGGCCCTATGTTCCCGCCACCTTCTCTGTACACG 831
Db 1033 GACCTGGTGAGCCGGACACGAGGTTATGACCTGTGTGGAGCCGGACGAGGTTACG 1092

Qy 832 CAGTCGTGGGAGGACCCCGACCGGATATGAGGTGATGGAGATCAACCCCAAGACACG 891
Db 1093 GACCTGGTGAGCTGGACACGAGGTTACGACCTGTGTGGAGCTGGGCTTGGAGTTACG 1152

Qy 892 GTGCTGACCTGACTAGCGGCGGCTGCATGCCCTGAACTCTGTGTGGAGCTGGACCTGGAGTTACG 951
Db 1153 GACCTGTGTGGAGCTGGACCTGGAGTTACGACCTGTGTGGAGCTGGACCTGGAGTTACG 1212

Qy 952 CAGGTGGTGTCCGTGGACTGCAACCCCGCGCAGTCGGCGCTTCTGGAGCTGAAGAAGTG 1011
Db 1213 GACCTGTGTGGAACTGGACCTGTGTGGATACGACCTGTGTGGAACTGGACCTGGAGATTG 1272

Qy 1012 GCCATTACGACGTGGAGTTTGGAGACGTGTGGAGCTGTTCGGCGAGGGCGTGAACCCG 1071
Db 1273 GACCTGGAGGAGCTGGACACGAGGATATGGACCTGTGTGTGTGGACCTGTGTGTGTG 1332

Qy 1072 CGCATTTAGGAGCTGTACGAGAAGAGCTGGCGCCTTCTCTG-TGCAAAACGACCAAA 1130
Db 1333 GACCTGTGTGTGTGGACCTGTGTGTGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1392

Qy 1131 CTTCTGTGTCCAAGCGCTCTGTACTTCCAGCAGCGCTGTACTACAGGCGCGATGGG 1190
Db 1393 GACCTGTGTGGATACGGCCCTGTGTGATCTGACCTGTGTGTGTGTGTGTGTGTGTGT 1452

Qy 1191 CAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1250
Db 1453 GACTTGTGTGT-GCTTGGACCTTGGAGTTCGGGACTTGTGTGTGTGTGTGTGTGTGTGT 1511

Qy 1251 CGGCTCGCCAAACCGGCCCAATGGAGGAGCAGCGCGCTGTGTGGACACCAATGCT 1310
Db 1512 GGAACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1571

Qy 1311 CATCCACTTCGTGAAGAACCGGCCCAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1370
Db 1572 GGACCCGCTGTGTGAGGACGTGGAGGACAGGTCTGTGTGTGTGTGTGTGTGTGTGTGT 1631

Qy 1371 CCTGTGTCTTCAACAAAGCCGTG 1395
Db 1632 GCTGTGTGAGGTGCAGGACGTGGTG 1656
```

RESULT 5
US-09-902-540-6564
; Sequence 6564, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6564

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LENGTH: 1691
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-6564

Query Match          3.2%; Score 63; DB 3; Length 1691;
Best Local Similarity 44.9%; Pred. No. 0.0024;
Matches 323; Conservative 0; Mismatches 390; Indels 6; Gaps 2;

Qy 659 AGCAGAAGCTGGAGCGGTGTGGAGCAGAAACACCCAGGTTTCATCCCTACGTGCGGT 718
Db 260 AGGTGCGCTGTGCCACCGCTGGCGCGAAGCTGCCCAACGCGCATGACATCAAGACGGCG 319

Qy 719 GGCTGCGCGCCCTTACTAGTGTGGATTGCGCCCTGCCAGCGTTGGCCACGCCCTGCG 778
Db 320 CGCTGCGCGCGGTGGACAGCTTTCGCGATGCTCTGCTGTC---AGGAGTGGCGCTGA 376

Qy 779 ACGAGGAGCGGTGGAGCGCGCCCATGTTTCCGCCCCACCTTCTGTACACGAGTCGT 838
Db 377 GCGAGGAGTCCAGCGCTGCTCATCTTCCGGCGGACACGCGGTGGGCACGCCCATCG 436

Qy 839 GGGAGGACCCCGACCGCGATATGAGGTGATGGAGATCAACCCCAAGACACGCTGTGA 898
Db 437 CGGAGGCGGTGGCGCTGGATGGCGTGTGTGTGGAGTGAACGTCAACGCCGAACGCCCGG 496

Qy 899 CCCTGACTAGCGCGGTGCAATGCCCTGAACCTGTGTCAGGGGCGCGCCAGGTGG 958
Db 497 ACGCGCTCAGCCACTGTGGCGTGGCGCGAGGTGAGGTGTTGACGGGCTCCGCGTTGA 556

Qy 959 TGTGCTGTGACTGCAACCCCGCGCAGTCGGCGCTTCTGGAGCTGAAGAAGGTGGCAATTC 1018
Db 557 AGGTGCCCCAGCCGAAGCCCGCGAGTGGGSCACGCCCGCGCGAGCAGGTG---AAGG 613

Qy 1019 AGCAGCTGGAGTTTGAAGACGTGTGGCAGCTGTTCGGCGAGGGCGTGCACCCGCGCATTC 1078
Db 614 TGCCTGTGGAGGCCCGGACCGCTGCGCGCGCTACGTGGCGCGCTGTGTGGAGAACGTGA 673

Qy 1079 AGGAGCTGTACGAGAAGAGTGGCGCTTCTGTGTGCAAAACGACCAACTTCTGCT 1138
Db 674 AGATTGGCCGCTCTCCGAGTGGATGAGNACCGGTGAAGCGCGCGCGGGGTGGCGGCA 733

Qy 1139 CCAAGCGCTCTGTGTACTTCCAGCAGCGCTGTACTACAGGGCGGCAATGGCAAGCTGT 1198
Db 734 TCAACAAGTGTGGATGTACCAACTACGTGAACCTGGAGTACGGGCGAGCGCTGCACG 793

Qy 1199 GCTGGGTGTCTCAGTGTGCTGCGCTGTGGGACTGTGGGCAAGACCGTCAAGCGCCTCG 1258
Db 794 CTTTCGACCTTGGAGAAGCTGGCCCGGTGAGGAGATTGTGTCCTGACGCGCGCGCGCG 853

Qy 1259 CCAAGCGCCCAACAAATGGAGGAGCAGCGCTCTGTGGGACAGCAACATGTCTATCCACT 1318
Db 854 AGAAGCTCAAGACGCTGGACGGCAAGACCGCTCTGTGGAGTACCTGTGTATCG 913

Qy 1319 TCGTGAAGAACGGGCCCAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1377
Db 914 CGGACAAAGGACCGGGCGCAGGCCCATCGTGTGCGTTCATGGCGCGCGGCGACAGCGAGTGT 972
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RESULT 6
US-09-902-540-8514
; Sequence 8514, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10

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; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8514
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8514

Query Match
Best Local Similarity 3.2%; Score 63; DB 3; Length 2034;
Matches 162; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 790 GTGAGCGCGCCCATGTTCCCGCCACCTTCTGTTACACGACGCTGTTGGGAGGACCC 849
Db |||||
QY 664 GAGGAGCGCGCTTCTGTTCTGCTGCGCAGCAGTGGCGCAGCGCTGAGCGCGC 723
Db |||||
QY 850 GAGCGCGATATGAGAGTATGAGATCAACCCCAAGGACACGCTCTGACCTGACTAGC 909
Db |||||
QY 724 GCGCTGTACGAGCGCTGCGTGAGCGCGCGCAGCTGACGTGCGCGCTGGAGCGGCG 783
QY 910 GCGCGCTGCAATGCTGAACTGCTGTGTCAGAGGCGCGCGCAGGTGGTGTGCTGAGC 969
Db |||||
QY 784 AAGGAGCGCGAGGAGCGCTTCTTCTGCTGAGGCGGAGCGCGCGCTGCGCGAGCAC 843
QY 970 TGCACCCCGCGCAGCTGCGCGCTTCTGAGCTGAGAGAGTGGCCATTACAGAGCTGAG 1029
Db |||||
QY 844 CTGGACGAGCTGAGTGGACGCTGGAGCACCTTGGCGCGAGTGGCGCGCGAAAGCTGCC 903
QY 1030 TTTGAGGACGTGTGCGAGCTGTTCCGCGAGGCGGTGCAACCGCGCATTTGAGGAGCTGTAC 1089
Db |||||
QY 904 ACGTACTGCTGTTGAGTGTGATGGAGCGGAGCGCGCTGCGCGCGCTGCGCGCTCC 963
QY 1090 GAGAGAGCTGGCGCCCTTCTCTGTCG 1116
Db |||||
QY 964 CACCGGAGCGAGCGGAGCTGTGCG 990

RESULT 7
US-09-902-540-489
; Sequence 489, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 489
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-489

Query Match
Best Local Similarity 3.2%; Score 63; DB 3; Length 2730;
Matches 323; Conservative 0; Mismatches 390; Indels 6; Gaps 2;

QY 659 AGCAGAGCTGGAGCGCGTGTGGAGCAGAACACCCAGGGTTGATCCCTACGTCGCGT 718
Db |||||
QY 1299 AGTGGCTGCGCCACCTGCGCGGCGAAGCTGCCACGATGATGACATCAAGCAGGCGG 1358
QY 719 GGTGCGCGCCCTTACTGTTGATGAGTGGCGCGCTGCCAGCGTTGGCCACGCGCTGCG 778
Db |||||
QY 1359 CGCTGCGCGCGGTGACAGCTTGGCATGCTGTGCTGTCCA---AGGAGCTGGCGCTGA 1415
QY 779 ACGAGGAGCGGTGGAGCGCGCGCCATGTTCCCGCCACCTTCTGTACAGCAGTGTG 838
Db |||||
QY 1416 GCGAGGAGTCCAGCGCGCTGCTCATCTTCCGCGGAGACACGCGGTGGGACGCGCCATCG 1475
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QY 839 GGGAGGACCCCGAGCCGATATGAGGTGATGAGATCAACCCCAAGGACACGTTGCTGA 898
Db |||||
QY 1476 CGGAGCGCGTGGGCTGGTGTGAGGTGAACCTCAGCGGAAACCCCGG 1535
QY 899 CCCTGACTAGCGCGGCTGCAATGCCCTGAACCTGCTGTCAGGCGCGCGCCAGGTGG 958
Db |||||
QY 1536 ACGCGCTCAGCCACTGGGCGTGGCGCGAGGTGAGCGTGGTACCGGGCTCCGCGTTGA 1595
QY 959 TGTGCTGAGTGAACACCCCGCGAGTCCGCGCTTCTGAGCTGAAGAAGGTGGCCATTC 1018
Db |||||
QY 1596 AGTGTCCCGCCAGCCGAGCTGGGACACGCGCGCGCGCGAGCGTG---AAGG 1652
QY 1019 AGCAGCTGAGATTGAGACGTTGTGGCAGCTGTTGCGCGAGGGCGTGCACCCGCGCATG 1078
Db |||||
QY 1653 TGCCTGAGGCGCGCGCGCGCTGCGCGCTACGTGGCGCGCTGTTGGAGAACGTGA 1712
QY 1079 AGGAGCTGTACGAGAGAGCTGGGCGCTTCTGCTGCGCAACACGACCAACTTCTGTT 1138
Db |||||
QY 1713 AGATTGCGCGCTTCTGCGAGTGGATGCAAGCCGCTGAAGCGCGCGCGGCTGGCGCA 1772
QY 1139 CCAAGCGCTCTGCTGTTCTCCAGCACGCGCTGTACTACAGGCGCGCATGGGCAAGCTGT 1198
Db |||||
QY 1773 TCAACACGCTGGTGGATGCTCACCACCTACCTGGAATACGGGCGCGCGTGCAG 1832
QY 1199 GCTGGGTGCTGACGTGCTGCGCGCTGTTGGGACTGGGCAAGACCGTCAAGCGCTCG 1258
Db |||||
QY 1833 CTTTCGACCTGGAGAGCTGGCGCTCAGAGATTGCTCGTACGCGCGCGCGCGCG 1892
QY 1259 CCAAGCGCGCCACATGGAGGAGCAGCGCGCTGTTGGGAGCAGCAATGCTCATCCACT 1318
Db |||||
QY 1893 AGAAGCTCAAGACGCTGGACGCGCAAGGACCGCGCTCTGGAGCTGGATGACCTGTTATCG 1952
QY 1319 TCGTGAAGAACGGCGCCCAAGCGCTGTTGGTGTGCTGTTCAAGTTCGTGAGCCTGTTG 1377
Db |||||
QY 1953 CGGACAGGACCGGCGCGAGCCCATGCTGCGTCTGCGCGCGCGCGCGAGCGGTG 2011

RESULT 8
US-09-902-540-897
; Sequence 897, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 897
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-897

Query Match
Best Local Similarity 3.2%; Score 63; DB 3; Length 6855;
Matches 162; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 790 GTGAGCGCGCGCCCATGTTCCCGCCACCTTCTGTTACACGACGCTGTTGGGAGGACCC 849
Db |||||
QY 665 GAGGAGCGCGCTTCTGTTCTGCTGCGCAGCAGTGGCGCGAGGCGCTGGAGCGCGCG 724
QY 850 GAGCGCGATATGAGAGTGTGAGATCAACCCCAAGGACACGCTGCTGACCTGACTAGC 909
Db |||||
QY 725 GCGCTGTACGAGGCGCTGCGTGGAGCGCGCGCGCAAGCTGACGCTGGCGCTGGAGCGGCG 784
QY 910 GCGCGCTGCAATGCTGTAACCTGCTGTTGAGGCGCGCGCGCGCGAGGTGTTGCTGTTGAGC 969
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Db 785 AAGAGGCGAGGAGCGCTCTTCTTCTGCTGAGGCGAGCGCGCTGGCCGAGCAC 844
Qy 970 TGCACCCCGCGAGTGGCGCTTCTGAGCTGAAGAAGTGGCCATTACAGAGCTGGAG 1029
Db 845 CTGGACGACGTGGAGTGAGCGACCTGGAGCACCTGGCGCGAGTGGCGCGAAGCTGGCC 904
Qy 1030 TTTGAGGACGTGTGCACCTGTTGGCGAGGCGGTGCACCGCGCATTTGAGGAGCTGTAC 1089
Db 905 ACGTACTCGCTGGTGGAGTTGATGGAGCGGACGCGCTGGCCGCGCGCTGGCCGCGTCC 964
Qy 1090 GAGAGAAAGCTGGCGCCCTTCTCTGTCTG 1116
Db 965 CACCGGAGCGAGCGGGAGCGTGTCTG 991

RESULT 9
US-09-881-165-4
; Sequence 4, Application US/09881165
; Patent No. 6632930
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; APPLICANT: BAILEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUANG
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/211,732
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
; OTHER INFORMATION: Organophosphate Hydrolase
US-09-881-165-4

Query Match 3.2%; Score 62.4; DB 3; Length 1082;
Best Local Similarity 44.6%; Pred. No. 0.003;
Matches 246; Conservative 0; Mismatches 306; Indels 0; Gaps 0;
Qy 1371 CCTGTGTCTTCAACAGGCGGTGCTGTGTTGGCGGGCGGTGCCGGGAAGCAGTA 1430
Db 515 CCAGAGCTCGTGTCAAGGCGCGCGCGCGCTCCCTCGCCACCGCGGTGAC 574
Qy 1431 CGCGTGTATCAAGCGGAGCGCATCCCATTTGAGAACTACATCGCGCGCACCATGGAGG 1490
Db 575 CACCCACACCGCGCTCCAGCGGAGCGGAGCAGCGCGCCATCTTCGAGTCCGA 634
Qy 1491 CGTGGCGGAGAACTCGCACGTGCGCAAGCAGAACTACTTCTACTACAACTCGCTCACCGG 1550
Db 635 GGGCTCTCCCGTCCCGGTGTGATCGGCCACTCCGACGACACCGACGACCTCTCCTA 694
Qy 1551 CAAGTTCCTGGCGGACAACTGCCCACTTACCTGGCGAGGGGGCTTCGCCACCTCAA 1610
Db 695 CCTCACCGCCCTCGCGCGCGCGGTACTCTCATCGGCCCTGACCACTCCGCACTCCGC 754
Qy 1611 GAGTGGCTGTGGCAACCTGACCGTCTCCACCAACTTCTTCATGGAGGAGCTCAAGC 1670
Db 755 CATCGGCTCGAGGACAAAGCGCTCCGCTCGCCCTCTCGCATCCGCTCCTGGCAGAC 814
Qy 1671 CGGCACCTACCAAGGTGATTCTGATGACCAAGTGGAGTGGTGGATATGCCCGTGGC 1730
Db 815 CCGCGCCCTCTCTCAAGGCGCTCATCGACCAAGGCTACATGAAGCAGATCCTCGTGTCT 874

Qy 1731 CAACGAGCTGSCCGAGTGCCTGGCCAAAGCAGGTTGCGCGCGCGCATCGTCATCTGSCG 1790
Db 875 CAACGACTGGCTTCTTGGCTTCTCTCTAGTGAACCAACATCATGACGATGATGGACCG 934
Qy 1791 CTCGCGCTCCCTCAGCCCGCCCTACGCGGAGCTGATCCAGAAGCGGGCTTCGACGTGCG 1850
Db 935 CGTGAACCCGAGCGCATGGCTTTCATCCGCTCCGCGTGTATCCGTTCTTCCGCGAGAA 994
Qy 1851 CTGATCCGCGCGCCACTCAGGCTACATGACCGGTCAACATGTACAGTCTCTTCTTA 1910
Db 995 GGGCGTGCAGGAGACCTTCGCGCGCATCACCGTACCAACCGCGCGCTTCTCTCTC 1054
Qy 1911 CATGCCCGCGC 1922
Db 1055 CCGACCTTCG 1066

RESULT 10
US-09-902-540-2993
; Sequence 2993, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2993
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2993

Query Match 3.2%; Score 62.4; DB 3; Length 1167;
Best Local Similarity 43.7%; Pred. No. 0.003;
Matches 340; Conservative 0; Mismatches 426; Indels 12; Gaps 1;
Qy 762 CGTTGGCCACGCTGACGAGGAGCGGTGGAGCGCGCCCATGTTCCGCGCCACCTT 821
Db 351 CTTGCACTACGCGCGCGGACGATTCGCTCAGGTGACCCCGTCTGTCATCGCTACCT 410
Qy 822 CTTGTACACGCGAGTCTGGGAGGACCCGAGCGCGATATGAGGTGATGGAGATCAACCC 881
Db 411 GCGCGCAGCATGCGGCGGAGCAGCGGAGCTGTGCGAGCACCTGAAGATCATCCAGGA 470
Qy 882 CAAGGACACGCTGTGACCTTGTAGTGGCGGTGCAATGCCCTGAACCTGTGGTGCA 941
Db 471 CGACATCAGCTTACATCCCTTGGCGCGCTGAAGGTTGACCTCAACGTCGCGCGCT 530
Qy 942 GGGGCGCGCGAGTGTGTGCTGAGTGCACAAACCCCGCGAGTCGGGCTTCTGGAGCT 1001
Db 531 GGCCTCGGCGCTGGAGGCGCGCTGCGCTTCGACTTCAGCCACGTCAGCAAGGTGGAGCC 590
Qy 1002 GAAGAAAGTGGCCATTACGAGCTGGAGTTTGGAGAGCTGTGGCA-----GCT 1049
Db 591 GGAGGCTTCCGAGAGTGGAGAGTGTGAGACGCGGCGGAGGCGCGCAGCTGGT 650
Qy 1050 GTTCGGCGAGGCGTGCACCGCGCATTTGAGAGCTGTACAGAAAGCTGTGGCGCCCTT 1109
Db 651 GTTGTGCGGCTGCGCGCGCGCTTGGCGGTGCTGCGCGCTCGGCGCAAGGTTGTGCC 710
Qy 1110 CTTGTGCAACACGACACAACTTCTGCTCAAGGCTCTGTGACTTCCAGACGCGCT 1169
Db 711 GGTGCGGCTGGCCACGCTGTGGCTGCGCTGTGATGTCGCGCAACTGCGGCGAGTGAGCA 770
Qy 1170 GTACTACAGGCGGCGCATGGGCAAGCTGTGTGGGTGCTGCAAGTGCCTTGGCGCGTGTCT 1229

Db 771 CAGGCGCTCCAAAGCCGCGGACTACTGCGCCAGGCTGCGGGCGCAGGCGTCGCGGTGGA 830
Qy 1230 GGGACTGGGCAAGACCGTCAAGCGCTCGCCAAACGCGGCCCAAAATGAGGAGCAGCGCG 1289
Db 831 GGTGCGGTGCCCATCTCGGGCGGCAACGCGCGCTCCCCACATGCCCCAGCTCCAGG 890
Qy 1290 TCTGTGGAGACAAATGCTCATCCATCTTGTAAGAACGGGCCCAAGCGCTGGTGTG 1349
Db 891 GCTGTGGCGCGGTGTCAGCTGACGACCGCGCGCTGGAGACCTTGGAGGGCGCTGGAG 950
Qy 1350 GCTGTTCGTGAAGTTCGTGAGCGTGGTCTCTTCAACAGCGCGTGTGTGTTGGGCG 1409
Db 951 TCGGCCCTCAGTCACTACCTCTTCGGCGCCACGAAACATCGACCGCGCGCGCTCGAGG 1010
Qy 1410 CGGCGTGGCGGCAAGCAGTACGCGCTGATCAAGGCGGACGCGCATCCCATTTGAAACTA 1469
Db 1011 CGGTCACGAGACATCTCCAACTCGCTGGCAGCACCAGCTGAACATCATCCGCGCT 1070
Qy 1470 CATCGCGGCACTGAGCGGCTGGCGAGAACTCGACGCTGGCGCAAGCAACTAC 1527
Db 1071 GGGACAGGCGGCATGGCGGAGTCTTCTCGCCAAAGCAGGTGGCGGTGAAGGGCTTC 1128

RESULT 11

US-09-902-540-362
; Sequence 362, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 362
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-362

Query Match 3.2%; Score 62.4; DB 3; Length 1250;
Best Local Similarity 43.7%; Pred. No. 0.003; Indels 12; Gaps 1;
Matches 340; Conservative 0; Mismatches 426; Indels 12; Gaps 1;
Qy 762 CGTTGGCCACGCCCTTGCAAGGAGCGCGTGGAGCGCGCGCCCATGTTCCCGCCACCTT 821
Db 434 CTTGACTACGCGCGCGGCGGACGAGTTCCGTCAGTGGACCGGTGTCATGCGCTACCT 493
Qy 822 CTTGACAGCAGCTGCTGGGAGGACCCGAGCGGATATGAGGTGATGAGATCAACCC 881
Db 494 GCGCGCCAGCATGCGCGGAGCAGCGGAGCTGTGCGAGCACCTGAAGATCATCCAGGA 553
Qy 882 CAAGGACAGCTGTGACCTGACTAGCGGCGGTGCAATGCCCTGAACCTGCTGTGCA 941
Db 554 CGATCAGTACATCACTTGGCAGCGCGCTGAAGGTAACCTCAACGTGCGCGCT 613
Qy 942 GGGGGCGGCGAGGTGTGTCGTGGAATGCAACCCCGCGAGTCGGCGCTTCTGGAGCT 1001
Db 614 GCGTGGGCGCTGGAGGCGCGCTGCGCTTCGATTCAGCCACGTCAGCAAGGTGGAGCC 673
Qy 1002 GAAGAAGTGGCCATTGAGAGCTGGATTGAGGAGCTGTGGCA-----GCT 1049
Db 674 GGAGCGCTGCGAAGCTGGAGCAGGTGCTGGAGACGCGCGCAGGCGCGCAGCTGGT 733
Qy 1050 GTTCGGGAGGCGGTGACACCGCATTTGAGAGCTGTACAGAGAAGCTGGCGGCCCTT 1109
Db 734 GTTGTGCGGCGTGGCGCGCGCGGTGCTGGCGGTGCTGGCGGCTGCTGCGCAAGGTTGTGCC 793

Qy 1110 CTTGTGCAAAACCAAGCCCAAACTTCTGTGTCAAGCGCTCTGGTACTTTCAGACAGCGCT 1169
Db 794 GGTGCGGCTGGCCACGCTGTGGCTGCCGTGTGACTGCCGCAACTGCGGCGAGGTGAGCCA 853
Qy 1170 GTACTACAGGCGGCGGCAAGCTGTGTGGTGTGTCAGCTGCTGGCGGTGGTGTCT 1229
Db 854 CCAGCGCTTCAAGCGCGGAGTACCTGGCCAGGCTGCGGGCGCAGGCGTCCGGCGTGA 913
Qy 1230 GGGACTGGGCAAGACCGTCAAGCGCTCGCCAAACGCGCCCAAAATGAGGAGCAGCGCG 1289
Db 914 GGTGCGGTGCCCATCTGCGGGCGGCAAGCGCGGTGCCCCACATGCCCCAGCTCCAGG 973
Qy 1290 TCTGTGGAGACAGCAATGCTCATCTTCTGTGAAGAACGGGCCCAAGCGCTGGTGTG 1349
Db 974 GCTGTGCGCGCGGTGACGCTGACGACCGCGCTGGAGGACCTGGAGGCGCTGGAGAC 1033
Qy 1350 GCTGTTGCTCAAGTTCGTGAGCGCTGGTCTTCAACAGGCGCGTGTGTGTTGGGCG 1409
Db 1034 TCGGCCCTCAGTCAGTACCTCTTTCGGCGCCACGAAACATCGACCGCGCGCGCTCGAGG 1093
Qy 1410 CGGCGTGGCGGCAAGCAGTACGCGCTGATCAAGCGGACGCGCATCCCATTTGAAACTA 1469
Db 1094 CGGTCACGAGACATCTCCAACTGCTGGGCGAGCAGCTGAACATCATCCGCGGCT 1153
Qy 1470 CATCGCGGCACTGAGACGCGTGGGCGGAGAACTCGCACGTCGCGCAAGCAAGAACTAC 1527
Db 1154 GGGACAGGCGGCATGGCGGAGTCTTCTCGCCAAAGCAGGTGGCGGTGAAGGGCTTC 1211

RESULT 12

US-09-902-540-7318
; Sequence 7318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7318
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7318

Query Match 3.2%; Score 62.2; DB 3; Length 3579;
Best Local Similarity 42.3%; Pred. No. 0.0039; Indels 9; Gaps 2;
Matches 474; Conservative 0; Mismatches 638; Indels 9; Gaps 2;
Qy 821 TCCTGTACAGCAGTCTGTGGAGGACCCCGAGCGCGATATGGAGGTGATGAGATCAACC 880
Db 1517 TCCAGGACGCAAGGTCTGGAGGCCAAGGACAGAGGCAAGCCGGAAGCCGGCAAGC 1576
Qy 881 CCAAGGACGCTGTGACCTGACCTGATAGCGCGGCTGCAATGCCCTGAACTGCTGTGTC 940
Db 1577 CGGCAAGTGGCTGCGAAGACCGCCCTACAACGCGGTGTGGCTTACGACAGGTCTGCA 1636
Qy 941 AGGGGCGCGCCAGGTGCTGTGCTGGACTGCAACCCCGCGCAGTCTCGCGCTTCTGGAGC 1000
Db 1637 AGCGCGCGGAGGCGCGGGCGAGGCAAGAGCGGTGGCTCGAATCAACCAAGA 1696
Qy 1001 TGAAGAAGGTGGCCATTGAGAGCTGGAGTTTGAAGGACGCTGTGGCAGCTGTTCCGCGG 1060
Db 1697 AGGCCACCATCCCAACCGCTGAAGAAGGCGCTGCTCGACGCGGTGTGAGGCGCTACCTCA 1756
Qy 1061 CGGTGACCCCGCGCATTTGAGAGCTGTACGAGAAAGAGCTGGCGGCCCTTCTGTCGCAAA 1120

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1757 ACCTGCCAAGGGTGAGAAAGCGGTGGAGATCGCTTCAAGCGCGCAACATCTACTACC 1816
1121 CCAGCCCAAACTTCTGGTCCAAAGCGCTCTGGTATCTCCAGACGGCTGTACTACGAG 1180
1817 GCCAACAACCACTTCCAGAGCGGTGCTGCGCTTTCAGCGAGATCGCGCTCGGCTACCCG 1876
1181 CGGCAATGGGCAAGCTGTGCTGGGTGCTGCAAGTGCCTGGCGGTGGTGGGACTGGGCA 1240
1877 AGTACAAGTTTCGAAAGCGCGAGCGCGCGGGGAGATCTCCGCCAACCTCATCTCGACT 1936
1241 AGACCGTCAAGCGCTCGCCAAACCGCCCAATGGAGGAGCAGCGCGCTGTGGGACA 1300
1937 GGTACCACTGCTGAGAGCACTACCGAAGGTGAACGAGTGGCGGGCGCTTCTACGCCA 1996
1301 GCAACATGC-----TCATCCACTTGTGTAAGAAACGGGCCCAAGCGCTGTGTGGTGT 1354
1997 ATGACAAGCTGGCGTGGGCAAGTTCCCGCAGCACCTGGCGAAGCTCATCGAGCAGTCT 2056
1355 TCGTCAAGTTCGTGAGCTGTGCTCTTCAACAAGCGCGTCTGTGTTTCGGCGCGCGG 1414
2057 CTTTCAAGCTCGTCAGCGAGCTGGAGGAGAAAGAGTTCGAAAGGCCCGCCGAGGCGT 2116
1415 TGGCGGGCAAGCAGTACCGCTGATCAAGGGCGGACGGCATCCCATTTGAGAACTACATCG 1474
2117 ACCTCGCTTCGTGAAGCACTTCCGCGAGACGGAGATCGCCGACTTGGCGCTTACAACG 2176
1475 CGCGCAACATGAGCGGCTGGCGAGAACTCGACGTGGCGGCAAGCAAGCACTTCTTACT 1534
2177 CGTCCGTGCACTACTACAAGCGAAGCGCTTGGATTAAGGCCATCGAGGTGCGCAAGGCC 2236
1535 ACAACTGCCTCACCGCAAGTTCTGCGCGCAACTGCGCCACCTACTCGCGGAGGCGG 1594
2237 TGTTCGCGAGTACCGCGCTTCCAGACACGTGCGGACTTCCATCTACCGAAGCGGAGG 2296
1595 CTTTTCGCCACCTCAAGAGTGGCGTGGTGAACAACCTGACCGTCTCCACCAACTTCTTCA 1654
2297 CGCTGGAGGCACTTGGCGACTTTCAGGACGCGCGGCAACGTAAGGCGCTTACGTGGCG 2356
1655 TGGAGGAGCTCAAGCGCGCACTTACACCAAGGTGATTTCTGATGACCACTGTGAGTGGC 1714
2357 GCTACGAGCGAGCTGCGGTGACAAGGGCAACGCGAAGCGCGTGTGGCGGCAAGAAGA 2416
1715 TGGATATCCCGTGGCCAAAGCTGGCGAGTGCCTGGCCCAAGCAGTTGCGCC--GG 1771
2417 AGCGGGCGCGGTGACACAAACAAAGCCCGGTGGTGCAGAAAGTGGACGAGTCCAAAG 2476
1772 CGCGCATCGTATCGGCGCTCCGCTCCCTCAGCCCGCCCTACGCCAGTGTATCCAGA 1831
2477 CGCAGGTGGCGCTCTTCAACCGCGCCACTTACCGAGAGGGCTTGGCCAGTGAAGCGG 2536
1832 AGCGGGCTTCGAGTGGCGTGCATCCCGCGGCACTCAGGGGTATCATGACCGCGTCA 1891
2537 CGCTGCGCAACCGGAGCACTTACCTGACGTGTGGCGCGCGGCAAGGACGCGCACGAA 2596
1892 ACATGTACAGTCTCTTACATGATGCCCGCGGAGGGCGCC 1932
2597 TCCGCTCTCCATCATCGACCTGACGGCCAAAGCGCGCC 2637

```

RESULT 13
 US-09-902-540-694
 ; Sequence 694, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 694
 ; LENGTH: 5656
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 ; US-09-902-540-694

Query Match 3.2%; Score 62.2; DB 3; Length 5656;
 Best Local Similarity 42.3%; Pred. No. 0.0042;
 Matches 474; Conservative 0; Mismatches 638; Indels 9; Gaps 2;

Qy	821	TCCTGTACAGCAGCTCGTGGGAGGACCCCGAGCCGGATATGGAGTGTATGAGATCAACC	880
Db	3573	TCCAGGACGCCAAGTGTCTGAGGCCAAGAGCAGACAGGGCAAGCCGAGCGGCAAGC	3632
Qy	881	CAAAGGACACGGTCTGACCCCTGACTAGCGCGGCTCAATGCCCCTGAACCTGTGTGTC	940
Db	3633	CGGCAAGTGGCTGCAGAACCGCCCTACAAACGCGGTGCTGGCCTACGACGAGTCTGCA	3692
Qy	941	AGGGGCGCGCAGGTGTCTGGTGAATGCAACCCCGCGCAGTCCGGCGCTTCTGGAGC	1000
Db	3693	AGCGGGCGAGGCGCGGGGAGGCAAGAGCGAGCGGTGGGCTCGGACATCAACAAGA	3752
Qy	1001	TGAAGAAAGTGGCCATTTACGACAGCTGGAGTTTGAGGACGTGTGGCAGCTGTTCCGCGAGG	1060
Db	3753	AGGCCACATCCCAACGCTGAGAAAGGCGTCTCGACGCGTGTGAGGCGCTACCTCAAGT	3812
Qy	1061	CGGTGACCCCGCGCATTTGAGAGCTGTACGAAAGAAAGTGGCGGCCCTTCTGTGCGAAA	1120
Db	3813	ACGTGCCCAAGGTTGAGAAGCGGTGGAGATCGCTTCAAGGCGGCCAACATCTACTACC	3872
Qy	1121	CCAGCCAACTTCTGGTCCAGCGCTCTGGTACTTCCAGCAGGCTGTACTACGAG	1180
Db	3873	GCCACAAACCACTTCGACGAGCGGTGTGCGCTTCAGCGAGATCGCGCTCGGCTACCCCG	3932
Qy	1181	CGCGCATGGGCAAGCTGTGTGGGTGTGCAAGTGCCTGGCGCGTGTGTGGAGCTGGGCA	1240
Db	3933	AGTACAAGTTTCGAAACCGCGAGCGCGGCGGAGATCTCGCCCAACTCATCTCTGACT	3992
Qy	1241	AGACCGTCAAGCGCTCCCAACCGCCCCCAATGGAGGAGCAGCGCGCTGTGGGAGA	1300
Db	3993	CGTACCACCTGCTCAGAGACTACGCAAGGTGAACGAGTGGCGCGCGCTTCTACGCCA	4052
Qy	1301	GCAACATGC-----TCATCCACTTGTGAGAAAGGGGCCCAAGCGCTGTGTGGCTGT	1354
Db	4053	ATGACAAGTGGCGGTGGGCAAGTTCCGCGACGACCTGGCGAAGCTCATCGAGCAGTCTGT	4112
Qy	1355	TCGTCAAGTTCTGAGCTGGTGTCTTCAACAAGGCGCTGTGTGGTTTCGGCGCGCGCG	1414
Db	4113	CTTCAAGTCTGTCAGCCAGCTGGAGGAGAAAGAGATTTCGAGAAAGCCCGCGAGGCGT	4172
Qy	1415	TGCGGGCAAGCAGTACGCGCTGATCAAGGCGGACGGCATCCCCATTTGAGAACTATCATCG	1474
Db	4173	ACCTCGCTTCTGTAAGGACTTCCCGCAGACGAGATCGCCGACCTTGGCGCTCTACACG	4232
Qy	1475	CGCGCAACATGAGCGGTGGCGGAGAACTCGCAGTGGCGCAAGCAGAACTACTTCTACT	1534
Db	4233	CGTCCGTCGACTACTACAAGCGGAAGCGCTTGGATAAGGCCATCGAGGTGGCGAAGCGCC	4292
Qy	1535	ACAACTGCCTCACCGGCAAGTTCTTGGCGGCAAACTTGCCCCACCTTACTTGGCGGAGCGG	1594
Db	4293	TGTTTCGCGAGTACCCCGCTCCAAAGCAGCTGTCGCGGACTCCATCTACGGAACCGGAGG	4352
Qy	1595	CTTTCGCGCACCTCAAGAGTGGGTGGTGAACAACCTGACCGTCTCCCAACCACTTCTTCA	1654
Db	4353	CGCTGGAGGCCATTTGGCGACTTCGAGGACCGCGGCGCAACGTACGAGGCTTACGTGCGCG	4412
Qy	1655	TGGAGGAGCTCAAGCGCGCACCTTACACAGGTGATTTCTGATGACCACTGAGCTGCG	1714
Db	4413	GCTACGAGCGCAGCTGCGGTGACAAGGGCAACGCGCAAGGCGGTGGTGGCGCAAGAAGA	4472

QY 1715 TGGATATGCCGTGGCCAAAGAGCTGGCGGAGTGGCTGGCCAAAGCAGGTTCGGCC---GG 1771
Db 4473 AGCGGGGCGGTGGAGCAGACAAAGCCGCGGTGTGAGAAAGTGGAGCAGGTCCAAGG 4532
QY 1772 GCGGCATCGTATCTGGCGCTCCGCTCCCTCAGCCCGCTTACCGCGAGCTGTATCCAGA 1831
Db 4533 CGAGGTGGCTCTTCAACGCGGCACCTACCGAGAGGCTTGGCCAGGTGAAGGCGG 4592
QY 1832 AGCGGGTTCAGCTGGCTGCATCCGCGCGCCACTCAGGGCTTACATGGACCGCGTCA 1891
Db 4593 CGCTCGCAACCGGAGCACTACCTGACGCTGTGGCCGCGCGAAGGACGCCGACGAA 4652
QY 1892 ACATGTACAGCTCTTCTACATGGCCGCGCGAAGGGCGCC 1932
Db 4653 TCCGCTCTCCATCATCGACCTGACGGCGCAAGAGCGCGCC 4693

RESULT 14

US-09-902-540-6237
; Sequence 6237, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6237

; LENGTH: 981
; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-6237

Query Match 3.2%; Score 61.8; DB 3; Length 981;
Best Local Similarity 49.8%; Pred. No. 0.0038;
Matches 156; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 1443 GCGGACGGCATCCCATTTGAGAACTACATCGCGCACCATGAGCGCGTGGCGGAGAA 1502
Db 246 GGACGGCAGCGGTACCTCAATCAGCTCATCTGTGGCGCAAGGCGCGCGCGGAGCC 305
QY 1503 CTCGACGTGCGCAAGCAGAACTACTTCTACTACAACTGCCTCACCAGCAAGTTCTCG 1562
Db 306 CCCGAGACGTTGAAGACGGACCCCGCTGGTGTACCCAGGGCGGCTCCGGGGACTTCTCTGGC 365
QY 1563 CGACAACCTGACCTACCTGCGGAGGCGGCGCTTCCGCCACCTCAAGAGTGGCGTGGT 1622
Db 366 GCCACCGCCGACATCCCTTGGCGAGCAGGCTTGGGGCTGGATTCGAAGGCGAGGT 425
QY 1623 GGACAACCTGACCGTCTCCACCAACTTCTTATGAGGAGGTCAAAGCGCGCACCTACAC 1682
Db 426 CTGCGCCATCTCGGCGACACGCCCGGAGGACGAAAGCGGAGAACGCGCGCGCACGT 485
QY 1683 CAAGGTGATTCGTATGGACCACTGGGACTGGCTGGATATGCCCGTGGCCAAAGCTGGC 1742
Db 486 CAAGCTGTGATGTCTGGGCAATGAGCTGTCTCTCGCAACCTCATCCCAACGAGCTGGC 545
QY 1743 CGAGTGCTTGCC 1755
Db 546 CAAGGGCTTCGAC 558

RESULT 15

US-09-902-540-1047
; Sequence 1047, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1047
; LENGTH: 13332
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1047

Query Match 3.2%; Score 61.8; DB 3; Length 13332;
Best Local Similarity 49.8%; Pred. No. 0.0058;
Matches 156; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 1443 GCGGACGGCATCCCATTTGAGAACTACATCGCGCACCATGAGCGCGTGGCGGAGAA 1502
Db 11288 GGACGGCAGCGGTACCTCAATCAGCTCATCTGTGGCGCAAGGCGCGCGCGCGAGCC 11347
QY 1503 CTCGACGTGCGCAAGCAGAACTACTTCTACTACAACTGCCTCACCAGCAAGTTCTCTCG 1562
Db 11348 CCCGAGACGTTGAAGACGGACCCCGCTGGTGTACCCAGGGCGGCTCCGGGGACTTCTCTGGC 11407
QY 1563 CGACAACCTGACCTACCTGCGGAGGCGGCGCTTCCGCCACCTCAAGAGTGGCGTGGT 1622
Db 11408 GCCACCGCGACATCCCTTGGCGGAGCGGCTGGGGCTGGATTCGAAGGCGAGGT 11467
QY 1623 GGACAACCTGACCGTCTCCACCAACTTCTTATGAGGAGCTCAAAGCGCGCACCTACAC 1682
Db 11468 CTGCGCATCTCTGGCGACACGCCCGGAGGACGAGGCGGCGCGCGCGCACGT 11527
QY 1683 CAAGGTGATTCGTATGGACCACTGGGACTGGCTGGATATGCCCGTGGCCAAAGCTGGC 1742
Db 11528 CAAGCTGTGATGTCTGGGCAATGAGCTGTCTCTCGCAACCTCATCCCAACGAGCTGGC 11587
QY 1743 CGAGTGCTTGCC 1755
Db 11588 CAAGGGCTTCGAC 11600

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Job time : 368 secs

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Run on: May 4, 2006, 19:00:04 ; Search time 953 Seconds
(without alignments)
8320.283 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atgggggtcggtcgtagcg.....gcgcgaagaagacaactaa 1947

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /SID85/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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 - 18: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq5.*
 - 19: /SID85/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	66	3.4	1577	18	US-11-096-568A-10906
2	64	3.3	2736	10	US-10-858-730-38
3	62	3.2	4770	13	US-10-496-351-3
4	62	3.2	82746	13	US-10-496-351-56
5	61.2	3.1	4773	18	US-11-100-356-55
6	61.2	3.1	5283	18	US-11-100-356-54
7	60.8	3.1	1325	18	US-11-096-568A-1077
8	59.6	3.1	1347	18	US-11-096-568A-12531
9	59.6	3.1	2799	18	US-11-100-356-53
10	57.8	3.0	1599	18	US-11-096-568A-26187
11	57.6	3.0	1444	18	US-11-096-568A-20988
12	57.2	2.9	1906	17	US-11-166-609-1
13	56.2	2.9	3513	10	US-10-858-730-142
14	56	2.9	4282	17	US-11-183-624-1

15	56	2.9	4282	17	US-11-183-624-3	Sequence 3, Appli
16	55.2	2.8	1243	18	US-11-096-568A-25531	Sequence 25531, A
17	55.2	2.8	88421	17	US-11-205-109-1	Sequence 1, Appli
18	55	2.8	14055	13	US-10-496-351-1	Sequence 1, Appli
19	54.8	2.8	88421	17	US-11-205-109-1	Sequence 1, Appli
20	54.6	2.8	1283	18	US-11-096-568A-23551	Sequence 23551, A
21	54.4	2.8	2472	18	US-11-100-356-32	Sequence 32, Appli
22	54	2.8	2025	17	US-11-167-048-2	Sequence 2, Appli
23	53.8	2.8	2403	11	US-10-649-457-4	Sequence 4, Appli
24	53.8	2.8	3639	18	US-11-100-356-33	Sequence 33, Appli
25	53.8	2.8	37507	10	US-10-522-037-2	Sequence 2, Appli
26	53.6	2.8	1182	18	US-11-096-568A-26293	Sequence 26293, A
27	53.6	2.8	1580	18	US-11-096-568A-20206	Sequence 20206, A
28	53.6	2.8	2466	18	US-11-100-356-31	Sequence 31, Appli
29	53.6	2.8	2873	17	US-11-136-527-2776	Sequence 2776, Ap
30	53	2.7	1292	18	US-11-096-568A-19003	Sequence 19003, A
31	52.8	2.7	1958	18	US-11-096-568A-26982	Sequence 26982, A
32	52.8	2.7	3387	17	US-11-091-883-183	Sequence 183, App
33	52.8	2.7	3439	17	US-11-000-888-851	Sequence 851, App
34	52.6	2.7	1572	18	US-11-096-568A-19140	Sequence 19140, A
35	52.6	2.7	1971	18	US-11-100-356-38	Sequence 38, Appli
36	52.2	2.7	645	13	US-10-496-351-6	Sequence 6, Appli
37	52.2	2.7	1672	13	US-10-943-508A-16	Sequence 16, Appli
38	52.2	2.7	1859	18	US-11-096-568A-25607	Sequence 25607, A
39	52.2	2.7	30191	11	US-10-330-773-631	Sequence 631, App
40	52	2.7	1401	18	US-11-096-568A-22550	Sequence 22550, A
41	52	2.7	3624	11	US-10-755-092-6	Sequence 6, Appli
42	51.6	2.7	2007	18	US-11-100-356-61	Sequence 61, Appli
43	51.6	2.7	2007	18	US-11-100-356-62	Sequence 62, Appli
44	51.6	2.7	2007	18	US-11-100-356-63	Sequence 63, Appli
45	51.6	2.7	2028	18	US-11-100-356-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1

US-11-096-568A-10906
; Sequence 10906, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10906
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1577)
; OTHER INFORMATION: Ceres Seq. ID no. 13597454
US-11-096-568A-10906

Query Match 3.4%; Score 66; DB 18; Length 1577;

Best Local Similarity 47.2%; Pred. No. 1.4e-06;
Matches 201; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

Qy 1408 GCGCGCGTCCGGGCAAGCAGTACGCGCTATCAAGCGGCGGCGCATCCCCATTGAGAAC 1467

Db 315 GGATACATGCGCGGCGCGCTCTACGACCTGACCGTCCAAGTACGGCACGCGGTGGAG 374

Qy 1468 TACATCGCGCGCACCATGAGCGGTGGCGGAGAACTCGACGTGCGGCAAGCAGACTAC 1527

Db 375 CTCAGTGTCTCATCGCGCGCTTCGTGTCGCAAGGCGCATCAAGTGTGCGCGCATCGTC 434

Qy 1528 TTCTTACTACACTCGCTCACCGGCAAGTTCTGTCGCGGCAACTGCCACCTACTCTGCGC 1587

Db 435 ATCAACACCGCTGCGCGGCGGAGCAAGACGCGGCGGCGCATCTACTGTCTTCAAGGCG 494

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QY 1588 GAGCGGCTTCGCCACCTCAAGAGTGGCGTGGGGAACCACTGACCGTCTCCACCAAC 1647
Db 495 GGAGACCCGAGGGGCTCTCTGGACTGGGGTCCGGGCATGATCTGCGAGCGACACCAAG 554
QY 1648 TTCTTCATGGAGGAGCTCAAGCGCGCACCTACACCAAGGTGATTCTGATGGACCACTG 1707
Db 555 TTCTCCGAGCGACGGGTACCGTGATACCGGCGGGAATTTCGGCGCGCGCCGACATC 614
QY 1708 GACTGGCTGGATATGCCCGTGGCCAAAGAGTGGCCGAGTGCCTGGGCCAAAGAGTTGCG 1767
Db 615 GACCACCTCAACCCGCGGTCCAGAAGGAGTCTCCGACTGGCTCAACTGGCTCAAGTCC 674
QY 1768 CGGCGCGCATGTCATCTGGGGTCCGCTCCCTCTCAGCCCGCCCTAGCGCGAGTGTATC 1827
Db 675 GACCTCGGCTTCGACGGGTGGCGCTCGACTTCGCCAAGGGGTACTTCGGCGGACGTGCC 734
QY 1828 CAGAAG 1833
Db 735 AGGACG 740

RESULT 2
US-10-858-730-38
; Sequence 38, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-38

Query Match 3.3%; Score 64; DB 10; Length 2736;
Best Local Similarity 47.6%; Pred. No. 4,1e-06;
Matches 221; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 1458 CATTGAGAACTACATCGCGCGCACCATGGACGGGTGGCGGAGAACTCGCACGTGCGCAA 1517
Db 1011 CACCAAGCAGCGCTTCGCCAAGGGCACCCCGACGAGGACGGCGCGACTACCTCGGCAC 1070
QY 1518 GCAGAACTACTTCTACTAACAATGCTCACCGGCAAGTTCCTGGCGCAACTGCCCCAC 1577
Db 1071 CGCCAGCTCATCGACGACCTGCGCATGTCAGACCTCGTGGCGCAACACCGCGGG 1130
QY 1578 CTACTCGCGGAGGGCGCTTCGCCACCTCAAGAGTGGCGTGGTG---ACAACTTCAC 1634
Db 1131 CTGTTTCGCGAGCGGCGCTTCGCCGACCATCATCGACCTTGGCGCTTCGCGCTCCA 1190
QY 1635 CGTCTCCACCAACTTTCTTCTGAGGAGGCTCAAGCGCGGCACTACACCAAGGTTGTTCT 1694
Db 1191 GCTCGCCACCATGGACGTCCGCGAGCAGCGCGACGCCCAACCAACGCGCTTCGGCAGCT 1250
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QY 1695 GATGCACACGTGACTGGCTGGATATGCCGTGSCCAACGAGCTGGCCGAGTGCCTGGC 1754
Db 1751 CTTGCAGCGGCTCGCGGAGGAGTCTCTGGCGGTACGCCGACATGCGCGCGAGTACCGCAC 1310
QY 1755 CAACGAGTGTGCGCGCGCGGCATCGTCACTGCGCGTTCGCGCTCCCTCAGCCCGCCCTA 1814
Db 1311 CAAGCTCTCGCCAAGNACTGCGCTCCCGCAGGCGCTGGCCCCCAGCCCCCGCCCGT 1370
QY 1815 GCGCGAGTGTATCCAGAAGCGGGCTTCGAGCTGGGTGCAATCCGCGCGGCACTCAGGG 1874
Db 1371 CGACGCGCGCGCGAGAAGACCTTCGCGGTCTTCAGACCGTTCGCGCGCGCCCTGGAGGT 1430
QY 1875 CTACATGGAACGCGCTCAACATGTATACGTCTCTTACATGSCCC 1918
Db 1431 CTTGCGGCCGAGGTATCGAGTCTTACATCATCTCCATGTGCC 1474

RESULT 3
US-10-496-351-3
; Sequence 3, Application US/10496351
; Publication No. US2006008414A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; TITLE OF INVENTION: Ansamitocin
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4770
; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-3
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Query Match 3.2%; Score 62; DB 13; Length 4770;
Best Local Similarity 44.9%; Pred. No. 1.2e-05;
Matches 236; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 1380 CTTCAACAAGGCGGTGTGTGTTTCGGCGGGCGGTTCGGGGCAAGAGTAGTACGCGCTGAT 1439
Db 3459 CGTCCGCGCACGTGGCCCGCCCTCGCGCCCTCGGCGCCGACCACTCTGCTCTCAC 3518
QY 1440 CAAGCGCGAGCGGCATCCCATTTAGAACTACATCGCGCGCACCATGAGCGCGGTGGCGGA 1499
Db 3519 CAGCGCGCGGCGCCCTCGGCCCCCGCGCGCGCTCGCGCCGACCTTGAGGCGCT 3578
QY 1500 GAACTCGCATGTGCGCAAGCAAGAACTACTTACTACATGCTCTCACCGGCAAGTTCCCT 1559
Db 3579 GGGCGCGCGGTACACACCGCCGCTCGAGTTCGCGACCGCGCGGCTTCGCGCCCT 3638
QY 1560 GCGCGAACAATCGCCCACTACCTGCGAGGCGGCGCTTCGCCACCTCTCAAGAGTGGCGT 1619
Db 3639 GCTGACCGCTTGAGCGCGCGGCGGAGCAGTCAACCGCGCTCTGTCACGCGGGGCGC 3698
QY 1620 GGTGGAACAACCTGACCGTCTCCACCAACTTTTATGAGAGAGTCTAAAGCGCGCACCTA 1679
Db 3699 CAACGCCAGACCCCGCTGCGCGCACCAACCCCGAGAGCAGCGCGCGCTCCAGGCGCG 3758
QY 1680 CACCAAGTGTATTGTATGGACCAAGTGTGCTGGATATGCCGTGGCCCAAGAGCT 1739
Db 3759 CAAGCGCTCGCGCGCAGCACCTCGACAGCTGCTGGCGGGCGCGCCGCTTCGACGCGGT 3818
QY 1740 GCGCGAGTGTGCGCAAGCAAGTGTGGCGGGGGGATCTCATCTGCGCGCTCGCGCTC 1799
Db 3819 GGTCTGTCTCTTCCAAACGCGGCGGTGTGGGCGAGCGGCGCGAGTGGCGCTACGCGC 3878
QY 1800 CCTCAGCGCGCCCTTACGCGAGCTTGATCCAGAAGCGGGGTTCGACGTTGCGCTGATCCG 1859
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Db 3979 CGCCAACGCCCGCTCGACGCACTGGCCCAAGCGCGCGCGCGACGCGCGCTCGCCAC 3938

Qy 1860 CCGCGCCACTCAGGGCTACATGACCGCGCTCAACATGTATACAGTCC 1905

Db 3939 CTCGTCGCGCTGGGCGCCTGGGACGCGCGCGCATGTCTCCAGCGCC 3984

RESULT 4

US-10-496-351-56/c

; Sequence 56, Application US/10496351

; Publication No. US20060084141A1

; GENERAL INFORMATION:

; APPLICANT: Floss, Heinz

; APPLICANT: Yu, Tin-Wein

; APPLICANT: Leistner, Eckard

; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent

; TITLE OF INVENTION: Ansamitocin

; FILE REFERENCE: UWASH-06712

; CURRENT APPLICATION NUMBER: US/10/496,351

; CURRENT FILING DATE: 2004-05-19

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 56

; LENGTH: 82746

; TYPE: DNA

; ORGANISM: Actinosynnema pretiosum

US-10-496-351-56

Query Match 3.2%; Score 62; DB 13; Length 82746;

Best Local Similarity 44.9%; Pred. No. 1e-05;

Matches 236; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

Qy 1380 CTTTCAACAGCGCGCTGTGTGGTTTCGGCGCGCGCGTCCGGCAAGCAGTACGCGCTGAT 1439

Db 68521 CGTCGCGCGCACGTGGCGCGCGCTCGCGCGCTCGGGCGGACCACTCGTCTCTCAC 68462

Qy 1440 CAAGGCGGACGGCATCCCCATTGAGAACTACATCGCGCGCACCATGGACGGCGTGGCGGA 1499

Db 68461 CAGCCGCGCGGCGCCCTTCGGCCCCCGCGCGCGCTCGCGCGGACCTGGAGCGCT 68402

Qy 1500 GAACCTCGACGTGGCGGACGAGAACTACTTCTACTACACTGCCTCACCGGCAAGTTCT 1559

Db 68401 GGGCGCGCGCGTCAACACCGCGCGCTCGGACGTTCGCGCGACCGCGCGCTCGCGCGCT 68342

Qy 1560 GCGCGCAACTGCCCCACCTACCTTCGCGGAGCGCGCTTTCGCCACCCTCAAGAGTGGCGT 1619

Db 68341 GCTACGCGCGCTGGAGCGCGCGCGGAGCAGGTCAACGCGCTGTGCAACGCGCGCGCG 68282

Qy 1620 GTGTGGAACCTGACCGTCTTCCAACTTTTCATGAGGAGAGCTCAAGCGCGCACTTA 1679

Db 68281 CAACGCGGACAGCCCCGTTCGCGACACCAACCCCGAGGAGACGCGCGCGTCCAGGCGC 68222

Qy 1680 CACCAGAGTGATTCTGATGGACCACTGGACTGGCTGGATATGCCCGTGGCCCAACGAGCT 1739

Db 68221 CAAGGCGCTCGGCGCGGACGACCTTCGACGAGTGTCTGGGCGGCGCGCTCGACGCGTT 68162

Qy 1740 GGCAGAGTGCTTGGCCAAAGCAGGTTCGCGCGGCGGCATGCTCATCTGGCGTTCGCGCTC 1799

Db 68161 CGTCTGTCTCTCTCAAACGCGGCGCTGTGGGCGACGCGGCGAGTGGCGCTTACGCCGC 68102

Qy 1800 CTTTACGCGCGCTTACCGCGAGTGTATCCAGAGGCGGGCTTCGAGTGGCGCTGCAATCG 1859

Db 68101 CGCCAAACGCGCGCTCGACGCACTGGCCCCAGCGCGCGCGCGCGCGTCCGCCAC 68042

Qy 1860 CCGCGGCACTCAGGGCTACATGGACCGCTGCTCAACATGTATACAGTCC 1905

Db 68041 CTGCGTCGCGTGGGCGCTTGGGACGCGCGCGCGCATGTCTCAGCGCC 67996

RESULT 5

US-11-100-356-55

; Sequence 55, Application US/11100356

; Publication No. US20060057115A1

```

; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 4773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: TatRevNefGagProteinartmut B
US-11-100-356-55

Query Match          3.1%; Score 61.2; DB 18; Length 4773;
Best Local Similarity 43.1%; Pred. No. 2e-05;
Matches 413; Conservative 0; Mismatches 533; Indels 12; Gaps 2;

QY 998 AGCTGAAGAAGGTGGGCCATTACAGCAGCTGGAGTTTGAGGACGTTGGCAGCTGTTCCGGCG 1057
      |||||
DB 1100 AGCTGTGTCCTGGACCCGACTAGCTGGAGGAGCCAAACCCGCGAGACACACAGCC 1159
QY 1058 AGGCGGTGCACCCGCGCATTTGAGGAGCTGTACAGAGAAGTGTGGCCCTTCTCTGTGC 1117
      |||||
DB 1160 TGTGTCAACCCTATGAGCAGCACGGCATGGACACCCCGAAGGAGGTGCTGGTGTGC 1219
QY 1118 AAACAGAGCACAACTCTTGTTCCAGCGGCTCTGTGTACTTCAGGACAGCCCTGTACTACC 1177
      |||||
DB 1220 GCTTGCAGACCGCCCTTGGCTTCCACCACATGCCCGCGAGCTGCACCCCGAGTACTACA 1279
QY 1178 AGGGCGGCATGGGCAAGTGTGTGTGGTGTCTGCAGTGCCTGGCCGTGTGTGGGACTGG 1237
      |||||
DB 1280 AGGACTGCAAGCTTGGCGCCCGGCCAGCGTGTCTGAGCGCGGAGCTGGACAGTGGG 1339
QY 1238 GCAAGACCGTCAAGCGCCTCGCCAAACGCGCCCAATAGGAGAGCAGCCCGTCTGTGGG 1297
      |||||
DB 1340 AGAAGATCGCCTGCGCCCGCGGCAAGAAGTACAAGCTGAAGCACATCGTGTGGG 1399
QY 1298 ACAGCAACATGTCTATCCACTTGTGTGAAGAACGGGCCCCAAGCCGTGGTGTGGCTGTTCCG 1357
      |||||
DB 1400 CACGCGCGAGCTGGAGCGCTTTCGCCGTGAAC---CCCGCCCTGTGGAGACACGCGAGG 1456
QY 1358 TCAAGTTCTGTAGCCTGTGTCTTTCAACAAAGCGGTGTGTGTGTGGCGCGCGGTGC 1417
      |||||
DB 1457 GTTGGCCGAGATCTTGGGCCAGCTGCAGCCAGCTGCAGACCCGCGACGAGGAGCTGC 1516
QY 1418 CGGGCAAGCAGTACCGCTGTATCAAGCGGCGACGGCATCCCCATTTAGAACTACATCGCGC 1477
      |||||
DB 1517 GCAGCCTGTACAACACCGTGGCCACCTCTACTGTGTCACACAGGSCATCGACGTTCAAGG 1576
QY 1478 GCACCATGACCGGTGGCGGAGAACTCGCACGTGGCGAAGCAGAACTACTTCTACTACA 1537
      |||||
DB 1577 ACACCAAGAGGCCCTTGGAGAGATCGAGGAGGAGCAGAAACAGTCCAAAGAAAGGCCCC 1636
QY 1538 ACTGCTCTACCGGCAAGTTCTTCCGCGCAACTGTCCCCACCTACCTGCGCGAGGGCGCT 1597
      |||||
DB 1637 AGCAGGCCCGCCCGCGCGCGCACCGGCAACAGCAGCCAGGTGAGCCAGAACTACCCCA 1696
QY 1598 TCGCCACCCCTCAAGAGTGGCGTGGTGGACAACTGACCGTCTCCACC-----AACT 1648
      |||||
DB 1697 TCGTGCAGAACCTGCAGGSCCAGATGGTGTGCACAGGCCCATCAGCCCCCGCACCCCTGAACG 1756
QY 1649 TCTTTCATGAGAGAGTCAAGCGCGGCACTTACACCAAGGTGATTTGTGATGGACACGTTGG 1708
      |||||
DB 1757 CTTGGGTGAAGTGGTGGAGGAGAAGGCCCTTCAGCCCCGAGGTGATCCCCCATTTTCAGCG 1816
      |||||

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QY 1709 ACTGGTGGATATCCCGTGGCCCAACGAGCTGGCGAGTGCCTGGCCNAGCAGGTTCGC 1768
Db 1817 CCCTGAGGAGGGCCACCCCCCAGGACCTGAACACAGATTTGAACACCCGTGGCGGCC 1876
QY 1769 CGGCGGCGATCGTATCTTGGCGCTCCGCTCCCTCAGCCGCCCTTAGCCCGAGCTGATCC 1828
Db 1877 ACCAGCGCCATGCAGATGCTGAAGGAGACCATCAACGAGGAGGCCCGCGAGTGGNACC 1936
QY 1829 AGAAGGGGGCTTCGACGTGCGCTGCATCCCGCGGCCACTCAGGGCTACATGACCGCG 1888
Db 1937 GCGTGCACCCCGTGCACCGCGGCCCATCGGCCCGCCAGATGCGGAGCGCCGCGGCA 1996
QY 1989 TCAACATGTACAGTCTCTTACATGGCCCGCGAGGGCGCCCAAGAGGACAATA 1946
Db 1997 GCGACATCGCGGCACCAACAGCCCTGACAGGACAGATCGGTGGATGACCAACAA 2054

RESULT 6
US-11-100-356-54
; Sequence 54, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100.356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190.434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: description
US-11-100-356-54

Query Match 3.1%; Score 61.2; DB 18; Length 5283;
Best Local Similarity 43.1%; Pred. No. 1.9e-05;
Matches 413; Conservative 0; Mismatches 533; Indels 12; Gaps 2;
QY 998 AGCTGAAGAAGTGCCATTACGAGCTGGAGTGTGAGGAGCTGTGGCAGCTGTTTCGCGC 1057
Db 1106 AGCTGGTCCCGTGGACCCCGACTACGTGGAGAGGCCAACCGCGCGAGAACACAGCC 1165
QY 1058 AGGCGGTGCACCGCGCATAGGAGCTGTACGAGAGAGTGTACGAGAGAAAGCTGGCGCCCTTCCTGTGC 1117
Db 1166 TGCTGCACCCCATGAGCAGCAGCATGGACGACGACCCCGAGAGAGGTGCTGTGTGC 1225
QY 1118 AACACGACCAACTTCTGGTCCAGCGCCTTGTGTACTTCCAGCAGCGCTGTACTACC 1177
Db 1226 GTTTCGACAGCGCGCTGGCCTTCCACCACATGGCCCGGAGCTGCACCCCGAGTACTACA 1285
QY 1178 AGGCGGCGATGGGCAAGCTGTGTGGTGTGCTGCACTGCTGCGCGTGTGTGTGGACTGG 1237
Db 1286 AGGACTGCTCAGGGCGCCCGCCAGCGTGTGAGCGGCGCGAGCTGGACAAAGTGG 1345
QY 1238 GCAAGACCGTCAAGCGCTTCGCCAAACCGCCCAACATGGAGGAGCAGCGCGCTGTGTGG 1297
Db 1346 AGAAGATCCGCTGCGCCCGCGCGCAAGAGAAAGTACAAGCTGAAGCACATCGTGTGG 1405
QY 1298 ACAGCAACATGCTCATCACTTCGTGAGAGAGCGGCCCAAGCCGCTGTGTGTGTTCG 1357
Db 1406 CCAGCCGAGCTGAGGCGCTTCGCGGTGAAC---CCGCGCTGCTGGAGACCAAGG 1462
QY 1358 TCAAGTTCTGTGAGCTGTGTCTTTCAACAAAGGCGGTGCTGTGGTTCGGCGCGCGCTGC 1417

Db 1463 GCTGCCCGCAGATCCTGGCGCAGCTGCAGCCAGCCTGCAGCCGCGCAGCGAGGAGTGC 1522
QY 1418 CGGCAAGCAGTAGTACGCGCTGATCAAGCGGACCGCATCCCCATTGAGAACTACATCGCGC 1477
Db 1523 GCAGCCTGTAAACACACCGTGGCCACCCTGTACTCGTGTGCACACGCGATCGACGTCAAG 1582
QY 1478 GCACATGGACGGGTGGCGAGAACTCGACAGCTGCGCAAGCAGAACTACTTCTACTACA 1537
Db 1583 ACACAGGAGGCCCTGGAGAGATCAGGAGGAGAGACAAAGTCCAAGAAAGAGGCC 1642
QY 1538 ACTGCCTCACCGCAAGTTCCTGCGGACAACTGCGCCCACTACTGCGCGAGCGGCT 1597
Db 1643 AGCAGGCGCGCGCGCCGCGCACCCGCAACCGCAACAGCAGCAGGTGAGCGCAGAACTACCCCA 1702
QY 1598 TCGCACCCCTCAAGAGTGGGTGTGACAACTGACCGTCTCCACC-----ACT 1648
Db 1703 TCGTGCAGAACCTGACAGGCGCAGATGTGTGCACCAAGGCCATCAGCCCGCGCACCTGAAACG 1762
QY 1649 TCTTCATGGAGGAGCTCAAAGCGCGCACCTACACAAAGGTGATTCTGATGACCAACGCTGG 1708
Db 1763 CTTGGTGAAGTGTGTGAGAGAGAGGCTTCAGCCCGAGGTGATCCCATGTTTCAGCG 1822
QY 1709 ACTGGTGGATATGCCGTGGCCAAACAGAGTGGCGGAGTGCCTGGCCAAAGCAGGTTCGCG 1768
Db 1823 CCCTGAGCGAGGGCGCCACCCCGCAGACCTTGAACACGATGTTGAACACCGTGGCGGCC 1882
QY 1769 CGGCGGCGATGCTATCTGGCGTCCCGCTCCCTCAGCCCGCCCTAGCCGAGCTGATCC 1828
Db 1883 ACCAGGCGCCATGACATGCTGAAGGAGACCATCAACGAGGAGCGCGCGAGTGGGACC 1942
QY 1829 AGAAGCGGGCTTCGAGCTGCGTGCATCCGCGCGCCACTCAGGGGTACATGAGACCGCG 1888
Db 1943 GCGTGCACCGCTGCACGCGGCCCATCGCCCGCCAGATCGCGCGCAGATCGCGCGCGCA 2002
QY 1889 TCAACATGTACAGTCTCTTACATGCGCCCGCGAAGGGCGCCAAAGAGCAACTA 1946
Db 2003 GCGACATCGCGGCACCAACAGCACCCCTGCAGGAGCAGATCGGTGGATGACCAACAA 2060

RESULT 7
US-11-096-568A-1077
; Sequence 1077, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1077
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1325)
; OTHER INFORMATION: Ceres Seq. ID no. 13599631
US-11-096-568A-1077

Query Match 3.1%; Score 60.8; DB 18; Length 1325;
Best Local Similarity 45.4%; Pred. No. 2.7e-05;
Matches 258; Conservative 0; Mismatches 307; Indels 3; Gaps 1;
QY 1218 GCGCGTGTGTGGGACTGGGCAAGACCGTCAAGCGCTTCGCCAACCGCGCCCAACAATGA 1277
Db 293 GCGGTGGGTTCGGCAAGCCAGCGCGCAGCGTGGCCGGATCCACGTGCCCGCCACATCGG 352
QY 1278 GGACAGCGCGCTGTGGGACAGCAACATGCTCATCCATTCGTGAGAGACGGGCCAA 1337
Db 353 CCTCCACCGCGCGACCTCGTGTGCGAGTGCTCATCAAGAAACCCCAACCCCGGTGCCAT 412

QY 1338 GCGCTGTTGGCTTTCGTAAGTTCTGTAGACCTGTGGTCTCTTCAACAAGGCGGTGCT 1397
 Db 413 CCGCTGTTGCTGATCGATACCTATCTACGACGACGCGCGGAAAGCTGTCGCGGGGT 472
 QY 1398 GTGGTTGCGCGCGGTGCGGGAAGAGTACGCTGA--TCAAGGCGGACGGCAT 1454
 Db 473 CATCCGGAGCGCGGACCATCGCGCGCAACGGGAGGAGCGGTCAAGGTGCCATCAC 532
 QY 1455 CCCCATTGAGAACTACATCGCGCGCACCATGACCGCGGTGGGAGAACTCGACGTGG 1514
 Db 533 GCTGACTTCGACGACATCCGGAGCACCTACCGGACATCAAGCGGGGAGCATATCC 592
 QY 1515 CAAGCAGAACTACTTCTACTACAACTGCTCACCAGCAAGTTCTCGCGGACAACTGGCC 1574
 Db 593 CTACCTGCTCCGGGTGATCTTCTCGTGACGTGCGCGCTTTCGCGCGCATCAAGATCCC 652
 QY 1575 CACCTACCTGCGCGAGGCGGCTTCGCCACCTCAAGAGTGCCTGGTGGACAACTGAC 1634
 Db 653 GCTGACAAAGTCCGGGAGATCCCATCCGTACAAAGCCCGAGCTGGAGCAAGAT 712
 QY 1635 CGTCTCCACCAACTTCTTCATGAGGAGCTCAAGCGCGCACCTACACCAAGGTGATTCT 1694
 Db 713 CAAGTTCCACCACTTCTCTTCGAGGAGACACGCGCACCATCCACCTGAGCTTGAGAA 772
 QY 1695 GATGACACAGCTGAGTGGCTGATATGCCGTGGCCAAAGAGCTGGCGAGTGCCTGGC 1754
 Db 773 CAAGAAGCACTTCGACCTCGGCTCAACCTGCTCAGTACGAGATGTGGCTCGGCGAGCA 832
 QY 1755 CAAGCAGGTTGCGCGGCGGCGCATGTC 1782
 Db 833 CAGCGTGTGGAGGCGGAGCTCACCGAC 860

RESULT 8
 US-11-096-568A-12531
 ; Sequence 12531, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 12531
 ; LENGTH: 1347
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(1347)
 ; OTHER INFORMATION: Ceres Seq. ID no. 14302247
 US-11-096-568A-12531

Query Match 3.1%; Score 59.6; DB 18; Length 1347;
 Best Local Similarity 47.2%; Pred. No. 5.2e-05;
 Matches 253; Conservative 0; Mismatches 274; Indels 9; Gaps 2;
 QY 1316 ACTTCGTGAGAACGGGCGCCCAAGCGCTGTGTGCTGTGCTGTTCTGTAAGTTCTGTGACCTGG 1375
 Db 351 ACAAGGTGACAGCGCTCAAGGACATGGCGGTGTGATGAAGCAGCGCGTTACCTGG 410
 QY 1376 TGCTCTTCAACAAGGCGGTGCTGTGCTGCGGCGGCGTGCCTGGGCAAGAGTACGGCG 1435
 Db 411 ACAGCGCGTGTGACGCGCATCCGCTGCTGCGCCACTCTGCCCGGGAGACAGTCCGAGG 470
 QY 1436 TGATCAAGCGGACGGC---ATCCCCATTGAGAACTACATCGCGCGCACCATGAGCGCG 1492
 Db 471 AGTCCCTGGACAAATCTCTGCTCGACCTTCAAGGCGCAGCGGCGCACCAAGGAGGAGA 530
 QY 1493 TGGCGGAGAACTGCGACGTGCGCAAGCAGAACTACTTCTACTACAACTGCTCTACCGGCA 1552

Db 531 TCGAGCTCTCAAGCACAAAGCTCCGCGGATCTACCAAGCGGCGGCTTCCCGCGCGGCA 590
 QY 1553 AGTTCTCTCGGAGCAAACTGCGCCCACTACCTGCGCGAGCGGCGCTTTCGCCAACCTCAAGA 1612
 Db 591 AGGCAC-----CAAGCGCGCGCTCCACGCGCGCAAGATCCACGCTCTCCGTCGAGC 644
 QY 1613 GTGGCGTGTGAGCAAACTGACCGCTCTCCACCACTTCTTATGAGGAGCTCAAGCGC 1672
 Db 645 AGGAGACGTCCCGGTGCTGGGCAACCTCGGTGGGCTTACATGACGAGCGCAACTTCA 704
 QY 1673 GCACCTACACCAAGGTGATTCTGATGAGACACGCTGACCTGGCTGATATGCCCGTGGCA 1732
 Db 705 TGGCGCGCGAGCGCTGTACCGCAAGGCGCAGATGTTGAGAGCGCCGCAACAAGGCT 764
 QY 1733 ACAGCTGCGCGAGTGCCTGCGCAAGCAGGTTGCGCGCGGCGGCACTCGTCACTCTGCGCT 1792
 Db 765 GCAACTCGCGCTGTGCTCATGAGCAGGCGGCGCTAGGAGACGCCGAGGGGTGCTCG 824
 QY 1793 CGCTCTCCCTAGCGCGCGCTTACGCGAGCTGATCCAGAAGCGGCGCTTCGACGTG 1848
 Db 825 CCGAGCTGTGCGCGCGCGCTTCCGCGACGCGGAGGAGGAGCAGCGCGCGG 880

RESULT 9
 US-11-100-356-53
 ; Sequence 53, Application US/11100356
 ; Publication No. US20060057115A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZUR MEGEDE, Jan
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: LIAN, Ying
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
 ; FILE REFERENCE: 2300-1621.20
 ; CURRENT APPLICATION NUMBER: US/11/100,356
 ; CURRENT FILING DATE: 2005-04-06
 ; PRIOR APPLICATION NUMBER: US/10/190,434
 ; PRIOR FILING DATE: 2002-07-05
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 53
 ; LENGTH: 2799
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: TatRevNefGag B
 US-11-100-356-53
 Query Match 3.1%; Score 59.6; DB 18; Length 2799;
 Best Local Similarity 43.0%; Pred. No. 5e-05;
 Matches 412; Conservative 0; Mismatches 534; Indels 12; Gaps 2;
 QY 998 AGCTGAAGAAGTGGCGCATTCAGGAGCTGTGAGGAGCTGTGGAGCTGTGGAGCTGTTCGGCG 1057
 Db 1100 AGCTGGTGGCGTGGACCCCGACTACGTGGAGGAGGCCAACCGCGCGAGAACAAACGCC 1159
 QY 1058 AGGCGCTGCACCGCGCATTCAGGAGCTGTACGAGAAAGCTGGCGCCCTCTCTGTGCGC 1117
 Db 1160 TGCTGCACCCATGAGCAGCAGCGCATGACAGACCCCGAGAGGAGGTGTGTTGTCG 1219
 QY 1118 AAACAGACCAAACTTCTGTGTCGAAGCGCTCTGTGATCTTCAGCAGCGCTGTACTACC 1177
 Db 1220 GTTTCGACAGCGCGCTGGCTTCCACCATGCGCGCGAGCTGCACCCGAGTACTACA 1279
 QY 1178 AGGCGCGCATGGGAAGCTGTGGGTGCTGAGTGTGCTGCGCTGCTGTGGAGCTGG 1237
 Db 1280 AGGACTGCGAATTCGGCGCGCGCGAGCTGTGCTGAGCGCGCGAGCTGGACAAAGTGG 1339
 QY 1238 GCAAGACCGTCAAGCGCTTCGCCAACCGCGCCCAAAATGGAGGAGCAGCGCGCTCTGTGG 1297
 Db 1340 AGAGATCCGCTGGCGCGCGCGCGCAAGAGTAACTGAAGCAGACATCGTGTGG 1399
 QY 1298 ACAGCAACATCTCATCTTCGTGAAGAAAGCGGCGCCCAAGCGCGCTGTGTGCTGTTCG 1357

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Db 1400 CCAAGCCGAGAGCTGGAGCGCTTCGCGGTGAAC---CCCGGCTGCTGGAGACCGAGG 1456
QY 1358 TCAAGTTTGTAGCCTGTGTCTTCAACAGAGCCGCTGTGTGGTTCGGCGGCGCGTGC 1417
Db 1457 GCTGCGGCAGATCTGGGCGCAGCTGCGAGCCAGCCTGCAGACCGGCAAGAGAGCTGC 1516
QY 1418 CGGCAAGACAGTACGCGCTGATCAAGGCGGAGCGCATCCCATTTGAGAACTACATCGCGC 1477
Db 1517 CGAGCTGTACAAACCGTGGCCACCTGTGCTGTGCACACAGGCGATCGACGTTCAAGG 1576
QY 1478 GCACCATGAGCGGCTGGCGGAGAACTCGCACGTGCGCAAGCAGAACTACTTCTACTACA 1537
Db 1577 ACACCAAGAGGCCCTGAGAGAGATCGAGGAGGAGCAACAAGTCCAAGAAGAGGCC 1636
QY 1538 ACTGCCTCACCGCAAGTTCTGCGCGAACAATGCCCCACCTACCTGCGCGAGGGCGCT 1597
Db 1637 AGCAGCGCGCGCGCCCGCGCACCGGCAACAGCAGCAGCGTGAAGCCAGAACTACCCCA 1696
QY 1598 TCGCCACCCTCAAGAGTGGCGTGGAGAACCTGACCGTCTCCACC-----AACT 1648
Db 1697 TCGTGCAGAACTGAGGGCCAGATGGTGACAGGCCATCAGCCCCGCAACCTGAAAG 1756
QY 1649 TCTTCATGAGGAGCTCAAAGCGCGCACCTACACCAAGGTGATTTCTGATGGACCACTGG 1708
Db 1757 CTTGGTGAAGTGTGAGGAGAGGCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCG 1816
QY 1709 ACTGGCTGGATATGCCCTGGCAACAGAGCTGGCGAGTGGCTGGCGCAAGCAGTTGGCG 1768
Db 1817 CCCTGAGCGAGGGCGCCACCCCGCAGGACCTGAACACGATGTTGAACACCGTGGCGCGCC 1876
QY 1769 CGGGCGCATCGTCATCTGGCGCTCGGCTCCCTCAGCGCCGCTTACGCGCAGCTGATCC 1828
Db 1877 ACCAGCGCCATGAGATGCTGAAGGAGACATCAACGAGAGCGCCCGAGTGGAGCC 1936
QY 1829 AGAAGCGGGCTTGACGCTGGCTGTCATCCGCGCGCCACTCAGGGCTTACATGGACCGCG 1888
Db 1937 GCGTGACCCCGTGACCGCGGCCCTTACGCCCCGCGCAGATGCGCGAGCCCGCGCA 1996
QY 1889 TCACATGTACAGTCTCTTACATGGCCCGCGGAGGGCGCCAGAGCAACTA 1946
Db 1997 GCGACATCGCGGCAACCAACGACCTCTGCAGGAGCAGATCGGTGGATGACCAACAA 2054
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RESULT 10

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US-11-096-568A-26187
; Sequence 26187, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096, 568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26187
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1599)
; OTHER INFORMATION: Ceres Seq. ID no. 13498780
US-11-096-568A-26187
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Query Match 3.0%; Score 57.8; DB 18; Length 1599;
Best Local Similarity 44.3%; Pred. No. 0.00014;
Matches 236; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

QY 1408 GCGGCGTGGCGGCAAGCAGTACGCGCTGATCAAGCGGCGGAGCGGATCCCCATTGAGAAC 1467
Db 277 GGGTACATGCGCGCGCGCTTCTACGACCTGGAGCGGTCCAAAGTACGGCACCCAGCGGAG 336
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QY 1468 TACATCGCGCGCACCATGGACGGCGTGGCGSAGAACTCGCACGTTGCGCAAGCAGAACTAC 1527
Db 337 CTAAGTGTCTTACCGGCGGTTTCAAGCCAAAGGGCGTCAAGTGTGCGTGGCGAGCGTGTG 396
QY 1528 TTCTACTACAACTGCTCTCACCGGCAAGTTCTTGTGCGGACAACTGCCCCACCTACTCTGCGC 1587
Db 397 ATCAACACACGCTGCGCGGACTACAAGGACGGCGCGGCATCTACTGCGTCTTCAGGGC 456
QY 1588 GAGCGGCGCTTGGCACCTCTCAAGAGTGGCGTGTGGACAACTGACCGTCTCCACCAC 1647
Db 457 GGCACGCGCGACAGCCGCTCGACTGGGGCGCCCGACATGATCTCGACGACGACACGCGAG 516
QY 1648 TTCTTTCATGAGGAGCTCAAAGCGCGCACCTTACACCAAGGTGATTTCTGATGGACACGCTG 1707
Db 517 TACTTCCAAAGGGCGGGGACCGGCGACAGGGGGCGGACTTCGCGCGCGCGCCGACATC 576
QY 1708 GACTGGCTGGATATGCCGTGGCCAAAGCAGTGGCCGAGTGGCTGGCCAAAGCAGGTTGCG 1767
Db 577 GACCACCTCAACCGCGCTGACGAGGAGCTCTCGGACTGGCTCAACTGGCTCAAGTCC 636
QY 1768 CCGGGCGGCATGTCATCTGGCGCTCGGCTCGCTCAGCCCGCTAGCCGAGCTGATC 1827
Db 637 GACCTCGGCTTCGACGGCTGGCGCTCGACTTCGCCAAAGGGCTACTCGCGCGCGTGC 696
QY 1828 CAGAAGCGGGCTTTCGACGTGCGCTGCATCGCGCGCCACTCAGGGCTTACATGGACCGC 1887
Db 697 AAGGTGATGCTGCACAGCACCGCCCCACCTTCTGCTGCGCGGAGATATGAGAGTCCCTC 756
QY 1888 GTCAACATGTACAGCTCTCTTACATGGCCCGCGGAAAGCGCGCAAGAGGA 1940
Db 757 CACTACGAGCGCAACGGGAGCGCTCCAGCAACCCAGGACGCGCGACAGCAGGA 809
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RESULT 11

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US-11-096-568A-20988
; Sequence 20988, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096, 568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20988
; LENGTH: 1444
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1444)
; OTHER INFORMATION: Ceres Seq. ID no. 12391561
US-11-096-568A-20988
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Query Match 3.0%; Score 57.6; DB 18; Length 1444;
Best Local Similarity 46.2%; Pred. No. 0.00016;
Matches 192; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 1527 CTTCTACTACAACTGCTCACCAGGTTCTCTCGCGGACAACTGCCCCACCTACTCTGCG 1586
Db 510 CTTCTGCGCTTACTTGCTCAGCTTCTGCACTGTGTGATATCTTCCCGGACCTCTCTGGG 569
QY 1587 CGAGGCGGCTTGGCCACCTCAAGAGTGGGTGGACAACTGACCGCTCTCCACCA 1646
Db 570 CGACCCGCGCTTACCGCGCGCGCAACACCTTCTTCTCATGGAACAAGGACAA 629
QY 1647 CTTCTTTCATGGAGGAGCTCAAAGCGCGCACCTACACCAAGGTGATTTCTGATGGACCACT 1706
Db 630 GGACTTCTGCTCTCTCGGAGCGGGCTCCACATCAAGCCCACTTCATCGGCAACA 689
QY 1707 GGACTGCTGATATGCCGTGGCCAAAGAGCTGGCGGAGTGCCTGGCCAAAGAGGTTGC 1766
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Db      690  CAACCCGGCCCTCAACCGGACATTACGTGGGTGAGGGCTGGGGGTACACTTCGTGCGC 749
Qy      1767  GCGGGCGGCGATCGTATCTTGCGGTCCGCTCCCTCAGCCCGCCCTACGCCGAGCTGAT 1826
Db      750  ACCAGCGCGCGCGGAGCCGACCGCTCTACGTCCGCGCGCGCAGGCGCGCGGATG 809
Qy      1827  CCAGAAGCGGGCTTCGAGCTGCGCTGTGANTCCGCGCGCACTCAGGGCTACATGAGCG 1886
Db      810  GGACGAGGAGGACGACCATCCAGCTCACCTTGAGCCGCGAGCCGCTCGAGCTCGAGC 869
Qy      1887  CGTCAACATGTACACTCTCTTACATGCGCCGCGGAGGCGCCCAAGAGGACA 1942
Db      870  COTCAAGAACGCGCGCTGGCGCTCCAGGCGCTCCCGGGGCTCTCCGTACACGGCA 925

RESULT 12
US-11-166-609-1
; Sequence 1, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1638)
US-11-166-609-1

Query Match      2.9%; Score 57.2; DB 17; Length 1906;
Best Local Similarity 43.1%; Pred. No. 0.0002;
Matches 275; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

Qy      908  GCGGCGGTGCAATGCCCTCAACCTGCTGGTGCAGGGGGCGCGCCAGGTGGTGGTGG 967
Db      911  GCGGCGGTTCGGGACGATAGAGCCTCCGGAGCTGGTGTCAACTTCGTGATCGCGC 970
Qy      968  ACTGCAACCCCGCAGTCGGGCTTCTGGAGCTGAAGAAGTGGCCATTGAGAGCTGG 1027
Db      971  GCGGGGACACGACGCGGACGAGCTGTCTGTGTTTACGCACATGGCCCATGTCCCA 1030
Qy      1028  AGTTTGAGGACGTGGGAGCTGTTTCGGGAGGGCGTGCACCCGCGCATTCGAGGAG 1087
Db      1031  ACGTGCGCGAGAAGCTGCGCGCGAGAGCTGTGCGGCTTCGAGCGGAGCGCGCGCG 1090
Qy      1088  ACGAAGAAGCTGGCGGCTTCTCTGTGCGAAACCCAGCACCAACTTCTGGTCCAAG 1147
Db      1091  AGGGGCTCAGCTGTGTCTTCGCGGCGGCTGACGCGCAGACAAAGCGTTCGCGCG 1150
Qy      1148  TCTGTACTTTCAGCACCGGCTGTACTACAGGGCGGCGATGGGCAAGCTGTGCTGG 1207
Db      1151  CGTGGCGAGTTCGCGGGCTCTCTACCTACGACAGAGCTCGGCAAGCTGTGTACT 1210
Qy      1208  TGCAGTGCCTGGCCGTGTGCTGGAGCTGGGCAAGACCGTCAAGGCCCTCGCCAC 1267
Db      1211  ACGCTGCGTCAACGAGAGCTCGCGCTGTATCCCGCGCTCCCTCAGGACCCCAAG 1270
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Qy      1268  CCACAATGGAGGAGAGCGCGCTCTGTGGGACAGCAACATGCTCATCCACTTCGTGA 1327
Db      1271  TCCTGGAGGACGAGCTGCTGCCGACGGAAGGTGAGGGCGCGGATGGTGAAGCT 1330
Qy      1328  ACGGCCCCAAGCCGCTGGTGTGGCTTTCGTCAAGTTTCGTGAGCCTGTGTCTTTCA 1387
Db      1331  ACGTGGCTTACTCATGGGGGCGATGGAGTACAATGGGGCCCCGACGCGGGAGCTTC 1390
Qy      1388  AGGCGGTGCTGTGTTCGGCGCGCGCTGTCGGGCAAGCAGTACGCGCTGATCAAGG 1447
Db      1391  GGCGGAGCGGTGATCAAGAGGATGGCGGTTTCGCAACGCGCTCGCGTTCAAGTT 1450
Qy      1448  ACGCATCCCATTTAGAACTACATCGCGCGCACCATGGAGCGGTGCGGGAGACTGC 1507
Db      1451  CGGCGTTTCCAGGCGGGCGGAGATCTGCCCTGGGCAAGGACTCGCGCTACCTGC 1510
Qy      1508  ACGTGCGCAAGCAGAACTACTTTACTACAACTGCCTC 1545
Db      1511  AGATGGCGCTGGCCATCTCTTCGCTTCTACAGCTTC 1548

RESULT 13
US-10-858-730-142
; Sequence 142, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 3513
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-142

Query Match      2.9%; Score 56.2; DB 10; Length 3513;
Best Local Similarity 44.6%; Pred. No. 0.00034;
Matches 266; Conservative 0; Mismatches 328; Indels 3; Gaps 1;

Qy      1146  CCTCTGTGTACTTCCAGCAGCGCTGTACTACAGGGGGCATGGCAAGCTGTGCTGG 1205
Db      1179  CCTCTGGTCACTACGTGCGCGCGGACGGCGTCCCGACATGAGGAACTGGCGGCG 1238
Qy      1206  GCTGCAGTGCCTGGCGCTGTGTGGGACTGGGCAAGACCGTCAAGCGCTTCGCCAAC 1265
Db      1239  GTTCGCCACCGCTCCACGCTGCCGATGCTCTCGACTCCACCAGGTTCGACGTCAT 1298
Qy      1266  GCCCAATGAGGAGAGCGCCCTGTGTGGGACAGCAATGTCTCATCTTCATTCGTGA 1325
Db      1299  GGCGGCGCTGGAGAAGCTCGGCGCGCGGTGATCAACTCGGTCAACTACGAGACGG 1358
Qy      1326  GAACGGGCCCAAGCGCTGTGTGTGCTTTCGTCGAAGTTCGTGAGCTGTGCTTTCAA 1385
Db      1359  GGCGGGCCCCGAGTCCCGGTTCCGCCCGCTCAGAACTCCCGCGGAGACGGCGCGC 1418
```

QY 1386 CAAGCGCTGTGTGGTTTCGGCGGGGTCTCGCGGCAAGCAGTACGCGCTGATCAAGGC 1445
Db 1419 GCTGATCGCGTGTACCATCGACGAGGTGGAGAGCCCGCACCGCGGAGAAAGGTGGA 1478
QY 1446 GGACGGCATCCCATTTGAGAACTACATCGCGCGCACCATGACGCGCGTGGCGGAGAACTC 1505
Db 1479 GATCGCGGAACGGCTCATCGACGACCTCACCGCAACTGGGGCATCCACGAGTCCGACAT 1538
QY 1506 GCAGTGGCGGAAGCAGAACTACTTCTACTACAATGCTCTACCGCGCAAGTTCCTGGCGGA 1565
Db 1539 CCTGCTGACTGCTGACTTTCACCATCTGCACCGGCC--AGGAGGAGTCCCGCAAGGA 1595
QY 1566 CAATGCGCCCACTACCTCGCGGAGGGCGCTTCGCCACCTCAAGAGTGCCTGTGGGA 1625
Db 1596 CGGCTGGCCACCATCGAGGGCATCCGGGAACTCAAGCGGCGCCACCGGACGTGCGAGAC 1655
QY 1626 CAACCTGACCGTCTCCACCAACTTCTTCATGGAGAGCTCAAGCGGCGCACTTACACCAA 1685
Db 1656 CACGCTCGGCCTGTGCAACATCTCTTCGGCCTCAACCGCGCGCCGCTCTGCTCAA 1715
QY 1686 GGTGATTTGATGACACACGTGAGTGTGCTGATATGCCGTGGCGCAACGAGTGGC 1742
Db 1716 CTCGCTCTCTCGACGAATCGTCAAGCGCGGCTGGACTCGGCCCATCGTGCAAGC 1772

RESULT 14

US-11-183-624-1
; Sequence 1, Application US/11183624
; Publication No. US20050255518A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; FILE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MP101-272P1RM
; CURRENT APPLICATION NUMBER: US/11/183,624
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/281,866
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4282
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: CDS
; LOCATION: (94)...(2859)
US-11-183-624-1

Query Match 2.9%; Score 56; DB 17; Length 4282;
Best Local Similarity 44.2%; Pred. No. 0.00038;
Matches 282; Conservative 0; Mismatches 350; Indels 6; Gaps 1;
QY 1024 CTGGAGTTTGAAGGACGTGTGGCAGCTGTTCCGGCGAGGGCGTGCACCCCGCATTTGAGGAG 1083
Db 766 CAGGTGTGGAGGCGCTGCTGACCTGTCTTCTCCCGTGTGGTGTATTCGCTCG 825
QY 1084 CTGTACGAGAAGAGCTGGCGCCCTTCTGTGCGAAACACGACCAAACTTCTGTGTCCAG 1143
Db 826 ATGGCCGACAAAGCGCTCTCTTCTACAAAGTACGTGTACAAAGCGCTACCGCACCGACCCA 885
QY 1144 CGCCTCTGTTACTTCCAGCAGCGCTGTACTACGAGGCGCATGGGCAAGCTGTGCTGG 1203
Db 886 CGCAGCGCATCATATAGGCGCGCAGGGCGACCCCGAAGAGCATCGAGCTGACGCG 945
QY 1204 GTGCTGCAGTGCCTGGCGTGTGTGGGACTGGGCAAGACCGTCAAGCGCTCGCCAAAC 1263
Db 946 ACCTTCGTGGCGCGAGGCCCGCCAGGTGAGTGTGGCGCGCTGGGCGCGGCCCGCGAG 1005
QY 1264 GCGCCCAAAATGGAGGAGCAGCGCGCTGTGTGGGACAGCAATGCTCATCTGCTGTG 1323
Db 1006 GCGGCGAGCTGGAGCGCGCAGCGCGGAGGTCTATCCAGATCCTCAAGGACCTCAAGCAG 1065
QY 1324 AAGAACGGGCCCAAGCGCGTGTGTGGTGTGTTCGTCAAGTTTCGTGAGCCTGTGCTTTC 1383

RESULT 15

US-11-183-624-3
; Sequence 3, Application US/11183624
; Publication No. US20050255518A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; FILE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MP101-272P1RM
; CURRENT APPLICATION NUMBER: US/11/183,624
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/281,866
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4282
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: CDS
; LOCATION: (94)...(2859)
US-11-183-624-3

Query Match 2.9%; Score 56; DB 17; Length 4282;
Best Local Similarity 44.2%; Pred. No. 0.00038;
Matches 282; Conservative 0; Mismatches 350; Indels 6; Gaps 1;
QY 1024 CTGGAGTTTGAAGGACGTGTGGCAGCTGTTCCGGCGAGGGCGTGCACCCCGCATTTGAGGAG 1083
Db 766 CAGGTGTGGAGGCGCTGCTGACCTGTCTTCTCCCGTGTGGTGTATTCGCTCG 825
QY 1084 CTGTACGAGAAGAGCTGGCGCCCTTCTGTGCGAAACACGACCAAACTTCTGTGTCCAG 1143
Db 826 ATGGCCGACAAAGCGCTCTCTTCTACAAAGTACGTGTACAAAGCGCTACCGCACCGACCCA 885
QY 1144 CGCCTCTGTTACTTCCAGCAGCGCTGTACTACGAGGCGCATGGGCAAGCTGTGCTGG 1203
Db 886 CGCAGCGCATCATATAGGCGCGCAGGGCGACCCCGAAGAGCATCGAGCTGACGCG 945
QY 1204 GTGCTGCAGTGCCTGGCGTGTGTGGGACTGGGCAAGACCGTCAAGCGCTCGCCAAAC 1263
Db 946 ACCTTCGTGGCGCGAGGCCCGCCAGGTGAGTGTGGCGCGCTGGGCGCGGCCCGCGAG 1005
QY 1264 GCGCCCAAAATGGAGGAGCAGCGCGCTGTGTGGGACAGCAATGCTCATCTGCTGTG 1323
Db 1006 GCGGCGAGCTGGAGCGCGCAGCGCGGAGGTCTATCCAGATCCTCAAGGACCTCAAGCAG 1065

Qy	1324	AAGAACGGGCCCCAAGCCCGCTGGTGTGGCTGTTGTCFAAGTTTCGTGAGAGCCTGGTGTCTTTC	1383
Db	1066	AAGCACCCGGACAGAGATCTGGAGCAGCTGTGGGCATCGCCAACTACTACGCGCTGCTG	1125
Qy	1384	AACAAGGCCGTGCTGTGTTTGGCGGCGGCGTGGCGGCAAGCAGTACGCGCTGATCAAG	1443
Db	1126	CACCAGCAGAAAGAGCCGCGCTTCTACCGCATCCAGGCCACGC-----GGCTGATGACC	1179
Qy	1444	GCGGACGGCATCCCCATTTGAGAACTACATCGCGCGCACCATGAGCGGCTGGCGGAGAAC	1503
Db	1180	GGCGCCGGGAACGTGCTCGGCAGACACCGGGGGAGCGCTCGCGCAGGGCGGCGCGGCC	1239
Qy	1504	TCGCACGTGCGCAAGCAGAACTACTTTCTACTACAACTGCTCCTCACCGGCAAGTTCTGTGCGC	1563
Db	1240	GAGGCGCGGCGAGGACGAAGACGACGGCGCCAGCCGCACTCTTTCGAGCCTAGCCTC	1299
Qy	1564	GACAACTGCCCCACCTACTCTGGCGAGGGGCGCTTCGCCACCCCTCAAGAGTGGCGTGTG	1623
Db	1300	TACCACCTGCCCTGGAGAACTGGGGCTCCGTGTGCTGTCCGTACGTGCCAGGGCGCGAG	1359
Qy	1624	GACAACTGACCGTCTCCACCAACTTCTTCATGGAGGA	1661
Db	1360	GGCAACAGCACCTTCTACTGTGACTACCGCACTGAGGA	1397

Search completed: May 4, 2006, 19:16:06
Job time : 955 secs

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GenCore version 5.1.7
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OM nucleic - protein search, using frameshifts-n2p.model

Run on: May 5, 2006, 07:49:43 ; Search time 7.4 Seconds
(without alignments)
4350.528 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

Sequence: 1 atggggctgggtcgtacgg.....gcgccaagaaggacaactaa 1947

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 segs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	374.5	10.3	663	2	US-09-252-991A-30843
C 2	352	9.7	310	2	US-09-248-796A-21233
C 3	332.5	9.2	663	2	US-09-252-991A-30843
C 4	332	9.2	536	2	US-09-252-991A-16754
C 5	326.5	9.0	681	2	US-09-252-991A-24567
C 6	324	9.0	2294	2	US-09-252-991A-17231
C 7	323	8.9	638	2	US-09-252-991A-27068
C 8	317.5	8.7	1706	2	US-09-252-991A-18296
C 9	316.5	8.7	1073	2	US-09-252-991A-31760
C 10	310	8.6	1073	2	US-09-252-991A-27341
C 11	309	8.5	798	2	US-09-252-991A-23774
C 12	308	8.5	1064	2	US-09-252-991A-17508

13	307.5	8.5	957	2	US-09-252-991A-20408	Sequence 20408, A
C 14	303	8.4	783	2	US-09-252-991A-18035	Sequence 18035, A
C 15	302	8.3	863	2	US-09-252-991A-26099	Sequence 26099, A
C 16	300.5	8.3	369	2	US-09-252-991A-25394	Sequence 25394, A
C 17	300	8.3	882	2	US-09-413-814-78	Sequence 78, Appl
C 18	299	8.3	511	2	US-09-252-991A-26078	Sequence 26078, A
C 19	298.5	8.2	720	2	US-09-252-991A-31915	Sequence 31915, A
C 20	298	8.2	568	2	US-09-252-991A-23264	Sequence 23264, A
C 21	297.5	8.2	885	2	US-09-252-991A-26129	Sequence 26129, A
C 22	295.5	8.2	885	2	US-09-252-991A-26129	Sequence 26129, A
C 23	295.5	8.2	1427	2	US-09-252-991A-29477	Sequence 29477, A
C 24	295.5	8.2	1476	2	US-09-252-991A-29427	Sequence 29427, A
C 25	295	8.2	686	2	US-09-252-991A-21221	Sequence 21221, A
C 26	295	8.2	783	2	US-09-252-991A-18035	Sequence 18035, A
C 27	295	8.2	882	2	US-09-413-814-78	Sequence 78, Appl
C 28	293.5	8.1	1008	2	US-09-252-991A-29419	Sequence 29419, A
C 29	291.5	8.1	631	2	US-09-252-991A-20063	Sequence 20063, A
C 30	291	8.0	801	2	US-09-252-991A-29274	Sequence 29274, A
C 31	290.5	8.0	1411	2	US-09-252-991A-28408	Sequence 28408, A
C 32	289	8.0	456	2	US-09-252-991A-19417	Sequence 19417, A
C 33	289	8.0	774	2	US-09-252-991A-16789	Sequence 16789, A
C 34	288	8.0	863	2	US-09-252-991A-26099	Sequence 26099, A
C 35	287.5	7.9	681	2	US-09-252-991A-24567	Sequence 24567, A
C 36	287.5	7.9	686	2	US-09-252-991A-20509	Sequence 20509, A
C 37	287.5	7.9	724	2	US-09-252-991A-31715	Sequence 31715, A
C 38	287.5	7.9	977	2	US-09-252-991A-16655	Sequence 16655, A
C 39	286.5	7.9	577	2	US-09-252-991A-25632	Sequence 25632, A
C 40	285.5	7.9	596	2	US-09-252-991A-18875	Sequence 18875, A
C 41	285.5	7.9	1053	2	US-09-252-991A-26140	Sequence 26140, A
C 42	284.5	7.9	691	2	US-09-252-991A-31413	Sequence 31413, A
C 43	284.5	7.9	1008	2	US-09-252-991A-29419	Sequence 29419, A
C 44	284.5	7.9	1520	2	US-09-252-991A-17501	Sequence 17501, A
C 45	283.5	7.8	419	2	US-09-252-991A-31734	Sequence 31734, A

ALIGNMENTS

RESULT 1
US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 2.18e-19 Length: 663
Score: 374.50 Matches: 211
Percent Similarity: 33.2% Conservative: 34
Best Local Similarity: 28.6% Mismatches: 231
Query Match: 10.3% Indels: 263
DB: 2 Gaps: 49

US-10-620-914-44 (1-1947) x US-09-252-991A-30843 (1-663)

QY 1771 CCGCGCAACCTGCTGCCAGGCACTCGGCCACCTCGTGGCCA-----CGGCATAT 1718

Db 4 ProalaproAlaIatrp-----ProGlnargItrProProArgalaala 19

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QY 1717 CCAGCCAGTCCA-----CGTGGTCCATCAGAATCA----- 1688
Db 20 ArgAlaSerProTrrpSerThrThrArgProProAlaAspArgSerGlyAlaThrAla 39
QY 1687 -----CCTTGGTGT-----AGGTGCGCGCTTTGAGTCTCT-----CCA 1655
Db 40 ArgValProAlaCysArgArgValProIleArgCysAlaAsnAlaTrrpProGlyArgPro 59
QY 1654 TGAAGAAGTTGGTAGACGCTGAGTTGTCCACACGCCACTCTTGAGGG----- 1604
Db 60 MetSerSerThrSerArgProGlyTrrpSerProAlaValProAlaGlyAlaCysCys 79
QY 1603 TGGCGAAGCGCCCTCGCGCAGGTAGG-----TGGGGCAGTTGTCGGCGCA 1559
Db 80 TrpIysThrArgAenValAlaGlyArgSerAlaThrAspAlaTrrpSerSerAlaProAla 99
QY 1558 ---GGAACCTTCGCGGTGAGGCAGTTGT-----CysCysLeuPheProAlaGlyProSerProAlaSerPro 116
Db 100 ProAlaAenCys-----CysCysLeuPheProAlaGlyProSerProAlaSerPro 116
QY 1528 AGTAGTTCTGCTTGGCAGCT-----GGGAGTTCTCCGCGCACGCCGTCATGG 1481
Db 117 AlaProAlaAlaCysArgArgTrrpProArgAlaAlaCysHisTrrpProAlaSerAlaTrrp 136
QY 1480 TGC-----GCGCGATGTAGTTCTCAATGGGATGCCGTCG-----CCTTGATCA 1436
Db 137 TrpTrpLeuAlaProAlaArgCysCys-----TrpProAlaProProAlaProAlaSer 154
QY 1435 CGCGGTACTGCTTGC-----CCGGCAGCGCGCGCCGAAACACAGCACGCGCTTGT 1385
Db 155 AlaGlyArgAlaCysCysAlaSerProAsnArgArgArgGluProTrrpProPro--- 173
QY 1384 TGAAGAGCACCAGGCTCAGAACTTGACGAACAGCCACAGCCAGCGGCTTGGCGCGTCT 1325
Db 174 -----SerProTyrAla----- 177
QY 1324 TCAGAGAGTGGATGAGCATGTTGTGTCCTCCACAGCGCGTGTCTCTCAATTGTTGGCG 1265
Db 178 SerArgAlaGlyProAlaSerCys-----GlyArgProPro----- 189
QY 1264 CGTTGGCAGGCGCTTGACGCTCTTTC-----CCAGTCCAGCACACCGCCAGGCACTGCA 1208
Db 190 -----AlaCysSerProValAlaThrAlaProThrAlaThrCys 202
QY 1207 GCACCCAGCACAGCT-----TGCCCATGCCCGCTCTGAGTACAGGC 1166
Db 203 SerProProSerAlaArgSerAlaTrrpIysProCysAlaCysAlaLys---AlaValGly 221
QY 1165 CGTGTGGAAGTACCAGAGGCGCTTGACCAAGATTGTGCTGTGTTGCGACAGGAAG 1106
Db 222 SerAlaArgSerProAlaAsnAlaTrrp----- 230
QY 1105 CGCGCAGCTTCTTCGTACAGCTCTCTCAATGCGCGGTGCACGCCCTCGCCGACAGCT 1046
Db 231 ---ProAlaAlaSerAlaTrrpCysProThrCysAsnSerAlaArgProSerAlaIleAla 249
QY 1045 GCCACA-----CGTCTCT-----CAACT 1028
Db 250 SerThrAlaArgArgSerProSerThrAsnGlyArgProAlaAlaCysProThrThr 269
QY 1027 CCAGTGTGTAATGGCCACCTTCTTCAGCTCCAGAGCGCGACTGCGCGGGTTGCAAGT 968
Db 270 ProProAlaAenAlaProAlaSerAlaAlaAlaAsnTrrpProTrrpIysAlaProSer 289
QY 967 CCACCGACACCACCTTGGCGCGCCCTTCACCA---GCAGGTTGAGGGCAATTGCAGCGCG 911
Db 290 ProAlaMetProProSerThrSerAlaThrArgLeuAlaAlaCysGlyHis----- 306
QY 910 CGTAGTCAGGTCAGCA-----CCGTGT 887
Db 307 -----AspGlyAspAlaGlyArgAlaSerGlnThrProTrrpArgAspThrSerProCys 324
QY 886 -----CCTTGGGCT-----TGATCT 872
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Db 325 ValProAsnCysValAsnTrrpArgArgIleProTrrpSerAlaValAlaLysThrSer 344
QY 871 CCATCACTCCATATCCGGCT-----CGGGTCTCT---CCACGACTCGCTGTACAGGA 821
Db 345 ProTrrpProArgTrrpProGlyMetProAlaGlyProArgProSerCysThrAlaValAla 364
QY 820 AGGTGGCGG-----GGAACATGGCGCGCGCTCCACGC---GTCCTCGTGCAGGG 773
Db 365 AlaTrrpAlaProAlaArgGlyGlyTrrAlaAlaAlaProArgAenSerCysSerAlaGly 384
QY 772 CGTGGCCAAAGC-----TGGCGAGGCGGC 749
Db 385 ArgLeuArgArgValArgSerAlaArgAlaTrrpArgProTrrpProAlaGly 404
QY 748 CAATCCACA-----CGTAGTAGGGGGCGCGCAGCCACG 716
Db 405 ArgAlaThrProAlaSerAspAlaArgAspSerAlaSerArgGlyArgProAlaThr 424
QY 715 GCAGTAGGGGATCGAACCCTGGGTGTTCTGCCACACGCGCTCCAGCTTCTGCCA 656
Db 425 AlaAlaAspHisProAlaAlaTrrpValSerAla---AlaArgArgThrSerSerAlaPro 443
QY 655 GGTAGGCGCGCGCTCGGGGCGCATGTCAATGTTGTGATGTGCAAGATCGATCGCCAGA 596
Db 444 IleAlaGlySerAlaProGlySerGlyThrAlaProArgCysHis----- 458
QY 595 AGAAACGGCGGACACAGGCATCTGGCGCAGGGCAGGTGCTACTTCCGCTCAGTAGA 536
Db 459 -----ProValArgLysAspGlyAlaGlyProAlaSerThrGlyArgSerArg 475
QY 535 AGTCGGCAACGCCACACAGGCGCTTGGGACAGGTACGACAGCTGGTTCGATGACGT 476
Db 476 ArgTrrpAlaAlaAlaProAlaArg-----ArgAlaArg 486
QY 475 TGTGGAACGGTGGAAATCATCTGTCGACGAGTAGGAGAAGGTGATGAGCGTCCGCTGCCCT 416
Db 487 ThrGlyLe-----ArgArgThrAlaAlaAlaCysTyr 498
QY 415 CAGGGGGCGCAAAATGGCAAGCGTCGGCTTCCA----- 383
Db 499 ProProAlaProGlyArgArgThrProAlaAlaArgArgArgSerAlaArgThrAla 518
QY 382 -----CGACCTGGACATTTCCAGCCCTTCCAGCTTCCAGTCCAC---CACCCA 230
Db 519 ProArgProAlaIleProAlaAlaHisArgProSerAlaSerAlaThrGlyTrrpProGlyPro 538
QY 346 TCTTCTTTGGCCACCTCGCACAGCGAGTGGCACAGGTCCACACAGTCCAGTGGACTTGAAC 287
Db 539 AlaLeuAlaCysProAlaAlaAla----- 546
QY 286 TCGCCAGCTCGATGTAATCAGCCATCATATCGACATTTCTCCCAAGTCCAC---CACCCA 230
Db 547 -----GlyArgArgProSerProAlaProAlaProAlaProAlaProHisAlaArgPro 564
QY 229 GGTCAACCCAGATGAGTTTCGAGCGCTCGGCGCAGCGCGGAGCAAGAGCGCGCTGGG 170
Db 565 ArgAlaProArg-----ArgArgProGlyArgSerProAlaAlaThrAlaProAla 580
QY 169 GCCCGTAGAAGCTCTCCAGGCGAGCAGCGTGCATCGCTTCTGCTGCCGAACCCACA 110
Db 581 Ala---PheAlaAlaProAlaGlyProThrProAlaArgProProAlaAlaAlaThr--- 598
QY 109 TATGGCGCAGAACCGTTCAGGTTCATCTTTCATGTGCTGAGCTTCTCCAGGGAGA 50
Db 599 -----GlyArgProSer-----AlaProArgProAlaArg 609
QY 49 AGTTCT-----TCTTGTGTAGCTCGCAGCGCGCGCTCAGCACCCGACCCCA 2
Db 610 ArgArgValArgTrrpProTrrpArgSerAlaArgCysSerProArgArgProThrPro 628
RESULT 2
US-09-248-796A-21233
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; Sequence 21233, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE OF INVENTION: 107196.132
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21233
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21233

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Pred. No.: 7,45e-18 Length: 310
Score: 352.00 Matches: 95
Percent Similarity: 40.5% Conservative: 35
Best Local Similarity: 29.6% Mismatches: 97
Query Match: 9.7% Indels: 94
DB: 2 Gaps: 8

US-10-620-914-44 (1-1947) x US-09-248-796A-21233 (1-310)

QY 430 CTCATCATTCTCTACTCGTTCAGATGATTCACCGTTCCACACGTCATCGACGAC 489
Db 3 LeuileThrPheSerTyrSerLeuSerMetileProThrPheAsnAlaileAspAsn 22
QY 490 GCTTCCTCGTACTCTCCACAGCGCTGGTGGCGTTCGCGACTTCTACGTAGC--- 546
Db 23 AlaValSerLysLeuAspMetGluGlyleileAlaThrValAspPheGlyleGlnSer 42
QY 547 -----GGCAAGTACGAC-----CTGCCCTCGCCAGATGCC 579
Db 43 SerAspThrSerMetGlyArgileAsnThrValGlyGlyLeuValAsnArgAspilePro 62
QY 580 TGGTCGCCCGTTCTTCTGGGATCGATCTTCGACATCGACACATGATGACGCGCCC 639
Db 63 TrpIleLeuArgAsnPheTrpArgileThrPheGluAlaAspLysValPheLeuAspSer 82
QY 640 GAGCGCGCGCTACTCGACGAGAGCTGGAGCGCGTGGAGCAGACACACCCAG--- 696
Db 83 SerArgArgAsnThrLeuGluThrLysPheGlyThrValLysSerLeuAsnSerTyrAsn 102
QY 697 -----GGTTCGATCCCTACGTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 747
Db 103 LysAlaLeuGlyLysleile-----ProTyrTyrIleTrpIle 114
QY 748 GCGCGCTGCCCGAGGTTGGCCACGCCCTGACGAGGAG-----CGCGTGGAG 795
Db 115 GlyCysAspLysSerLysSerHisThrileLeuGluArgLeuAsnCysLeuAlaThrGlu 134
QY 796 CGGCGCCCATGTTCCCGCCCGC-----819
Db 135 SerProTyrLeuAlaProThrThrThrProIleAlaAsnGlnLeuGluAspileProIle 154
QY 819 -----819
Db 155 SerLysGlyHisGluAlaAlaLeuIleAsnLeuGlnLysAsnLeuProTyrProSerMet 174
QY 819 -----819
Db 175 TyrTyrGlnLysGluTyrTrpArgValTyrTyrAspGluMetAsnProLeuTyrGluGln 194
QY 820 -----TTCCTGTACACGAGTCGTGGGAGGACCCGAGCGCGATATGAGGTG 867
Db 195 PheLysAsnGlnTyrIleTyrAlaPheThrThrLysAspProArgGluAspHisLysLeu 214
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RESULT 3

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US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 2.81e-16 Length: 663
Score: 332.50 Matches: 193
Percent Similarity: 32.4% Conservative: 52
Best Local Similarity: 25.5% Mismatches: 253
Query Match: 9.2% Indels: 259
DB: 2 Gaps: 44

US-10-620-914-44 (1-1947) x US-09-252-991A-30843 (1-663)

QY 29 CGAGCTACACCAAGA-----AGAACTTCTCCCTGGAGAAGCTCA----- 67
Db 12 ArgTrpProAlaArgAlaAlaArgAlaSerProThrSerThrThrThrArgProPro 31
QY 68 -----AGCTCAGCAGCATGAAGGATdACCTGACCGTTCCTCGCCCATATGTGTTCG 118
Db 32 AlaAspArgSerGlyAlaThrAlaArgVal-----ProAlaCys----- 44
QY 119 GCACAGAGAGGGCGATGATCAGCTGCTC---GCCTGG-----AGAGCTTCT 163
Db 45 -----ArgArgValProIleArgCysAlaAsnAlaThrProGlyArgProMetSerSer 62
QY 164 ACGGGCCCCAGCGCGCTTTGCTGCGCCCTGGCGAGCGCTCGAAACCTCATCTGGG 223
Db 63 ThrSerArgArg-----ProGlyTrpSerProAlaValProAlaGlyAla 77
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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16754
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16754

Alignment Scores:
Pred. No.: 2,8e-16 Length: 536
Score: 332.00 Matches: 181
Percent Similarity: 33.1% Conservative: 34
Best Local Similarity: 27.9% Mismatches: 193
Query Match: 9.2% Indels: 241
DB: Gaps: 36

US-10-620-914-44 (1-1947) x US-09-252-991A-16754 (1-536)

QY 1888 CGGGTTCATGTAGCCCTGAG-----TGGCGCGCGGTGCGAGCGCAGCTCGA 1841
Db 8 ArgArgProSerProProSerSerAlaSerAlaTrpSerAlaAlaSerSerMetPro 27
QY 1840 AGCCCG-----CCTTCTGGATCA 1823
Db 28 SerProAlaAlaAlaArgLysProAlaSerThrSerSerAlaSerAlaSerAlaSer 47
QY 1822 GCTCGGCGTGGCGGGCTGAGGAGCGG-----AGCGCCAGATGACGA----- 1778
Db 48 AlaAlaArgArgPro-----GlyArgArgProIleAlaCysAlaAArgTrpArgArgSer 65
QY 1777 TGGCGCGCGGCCAACCTGCTTGGCCAGGCACTCGGCAGCTCGTGGCCACGGGCATAT 1718
Db 66 CysArgProThrProSerCysTrpLysProMetArgArgThrTrpArgHisArgCysIle 85
QY 1717 CCAGCCAGTCCA-----CGTGTCCATCAGAATCACCTTGGTGT 1679
Db 86 ProAlaSerAlaThrValArgSerThrCysArgThrSerAlaAlaProSerProSerCys 105
QY 1678 AGTGGCGCGCTTTGAGCTCTCCATGAAGAAGTTGGTGGAGACGGTCAGGTGTGCCACCA 1619
Db 106 -----AlaGlySerThrPro 110
QY 1618 GGCACACTCTTGAGGGTGGCGNAG-----CCGCTCGCGCAGGTAGGTGG 1574
Db 111 ArgAsn-----TrpArgArgAlaAlaAlaThrProPro----- 122
QY 1573 GGCAAGTTGTGCGCAGCAACT-----TGCGGTGAGGCAGTTGT--- 1535
Db 123 ---SerCysSerAlaGlyThrAspGlnAlaSerArgArgThrSerGlyAlaSerCysGly 141
QY 1534 -----AGTAGAAGTAGTTCTGCTTGGCACAGTGGCAGTTCTCCGCCA 1493
Db 142 TyrValSerArgAsnAlaSerArgGlnAlaAspSerCysAla---AlaSerSerGlyArg 160
QY 1492 GCGCGTCCATGTCGCGCGCATGTAGTTCCTCAATGGGGATGCCGCTCGCTTGATCAGCG 1433
Db 161 ArgArg-----Ala 163
QY 1432 CGTACTGCTTCCGCGCACGCCGCCGCGCAACCAACACAGACCGGCTTGTGAAGACCA 1373
Db 164 LysSerLeuGlnProCysA-ArgAsnArg-----ArgGlyIle 176
QY 1372 GGGTCACGAAGTTGACGAACACCAACACACAGCGCTTGGGCCCGCTTCTCACGAAGTGA 1313
Db 177 GlyThrArgProLeuMetAlaSerGlnLysAlaSerGlnLeuHisProTyrHisGlyGly 196
QY 1312 TGAGCATGTTGCTGCTCCACAGACGGCGCTGC-----TCCT 1277
Db 197 --AsnAlaAArgAlaSerArgArgArgSerCysLysArgAlaAlaLeuSerThrSerAla 216

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Db 450 GlyProAlaThrSerLeuAlaasp---ProAlaArgProAlaAlaProArgArgArgLeu 468
Qy 628 CAATGTGTGTCGATCGAAGATCGATCGCCAGAGAAACGGCGCAGGCGCATCTGCG 569
Db 469 ProAlaLeuProAlaThrArgAlaAlaProAla---GlyAlaGlyGlyGlnSerArg 487
Qy 568 GCAGGGGAGGTGCTACTTGGCGCTCAGCTGAAGTGGCAAGCGCCACCGCGCTCTT 509
Db 488 LeuGlyAlaGlyHisArg---ArgGlyProArgHisArgAlaArgProAlaArg--- 505
Qy 508 GGGACAGGTACGAGCAAGCGCTGTCGATCGATGTCGGAACGGTGGATCATCTGTCGAGG 449
Db 506 GlyThrGlyThrProPro-----SerAlaGlyThrProArgAlaAlaLeuArg 521
Qy 448 ACTAGGAGAAGGTGATGAGCGTCGCGTCCCTCAGGGGGCGCAATTGGCAAGCGTCGG 389
Db 522 AlaAlaArgArg-----ThrLeuArgAlaPro---GlyAlaMetAlaGlyGlyArgHis 538
Qy 388 CCTCCACGACCTGGACATCTTCCAGCCCTTGGCCTTGGCCTCTCTTGGCCACTCGC 329
Db 539 -----GlyHisGlnHisProArgProAlaGlu-----ProValArg 551
Qy 328 ACAGCGAGTGGCACAGGT-----CGACCACGTAGATGGACTTGAACCTTCGCCA 281
Db 552 LeuValAlaGlyProGlyHisProLeuAlaArgProArgArg-----ThrPro 567
Qy 280 GGTGATGTAATCAGCCATCATATCGACATTTCTCCCGCAGTGCACCCAGGTCAACCC 221
Db 568 GlnArg-----ArgGlyMetArgGlyArgProGlyThrAlaArgArgGlyAlaPro 584
Qy 220 AGATGAGTTGAGCGTCCGCGCAGCGGGCGGCAAGAGCAGCGCTGGGGCCCGTAGA 161
Db 585 GlyProGlyArgGlnProArgThrAlaGlyArgSerArgProArg-----ArgArg 601
Qy 160 AGCTCTCCAGGCGCAGCGTGCATCTGC-----CCTTCTTGTGTCGCGA 116
Db 602 SerThrAlaGly-----ArgLeuHisArgLeuCysArgGlyAsnProArgAlaValGly 619
Qy 115 ACCATATGGCGCAGAACGGTCAGGTCACTTCCTCATCTGCTGCG----- 74
Db 620 AlaThrAlaProGlyGlyArgProGlyGlnProGlyAlaAlaGluProAlaArgProArg 639
Qy 73 -----TGAGCTTGACCTTCTCAGGGAGAGTCTTCTTGTGTAGCTCG 29
Db 640 ArgArgProProGluLeuAlaAlaAlaLeuAlaGlyLysArgArgAlaAspAlaArgAsn 659
Qy 28 CAGGCGGCGCTCAGCACCCGCCACCCCA 2
Db 660 AlaAlaGlyArgProAlaProAlaPro 668

RESULT 6

US-09-252-991A-17231
; Sequence 17231, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17231
; LENGTH: 2294
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17231

Alignment Scores:

Pred. No.: 1.97e-15 Length: 2294
Score: 324.00 Matches: 274
Percent Similarity: 29.3% Conservative: 43
Best Local Similarity: 25.3% Mismatches: 280
Query Match: 9.0% Indels: 485
DB: 2 Gaps: 58
US-10-620-914-44 (1-1947) x US-09-252-991A-17231 (1-2294)
Qy 20 GCCGCGCTCGCAGCTACACCAAGAAAGAACTTCTCCCTCG----- 58
Db 55 AlaGlyHisArgGlnArgProArgArgAlaAlaGlyTyrAlaValGlnHisProArg 74
Qy 59 ---AGAACTCAAGCTCAGCAGCA-----TGAAGGATG 88
Db 75 ArgArgSerGlyAlaGlyAlaAlaGluCysArgGlyLysProAlaArgTrpHisArgLeu 94
Qy 89 ACCTGACCGTTCTGCGCCATATGTTGTCGCGCAGCAAGAGGCGCATGTCACGCTGCTC 148
Db 95 ProArgPro---AlaAlaGluAlaGlyArgHisProArgHisGly----- 108
Qy 149 GCCTGAGAGCTTCTACGGCGCCCGCAGCGCTGCTTGTGCTGCGCGCTCGG----- 200
Db 109 -----ArgGlyGlyArgGlyProArgArgArgProLeuArg-GlnProGlyAlaGlySe 126
Qy 201 -----CGAGCGCTCGAACCTCATCTGGTTCGACTGGTGGTGGTGGCCTG 244
Db 126 rAlaArgArgGlnCysArgLeuArgGluProArgProGlyGlyProGly----- 142
Qy 245 GGGAGATGTCGATATGATGCTGATCATCGACCTCGCGAAGTTCAAGTCCATCTACG 304
Db 143 -----GlnProGlyValProProAlaAspArgAl 152
Qy 305 TGGTGCACCT-----GTGCCACTCGCTGTCGAGG 334
Db 152 aArgArgProArgArgIleArgArgGlyGlyArgArgAlaGlyProArgGluAlaArgG 172
Qy 335 T---GGCCAAAGAAAGCGAAGG-----CAAGGCTTGAAGAATGT----- 374
Db 172 yProGlyProGluProGlyArgGlyLeuProAlaAlaGlyAlaArgHisCysArgArgAl 192
Qy 375 -----CCNGTCTG----- 383
Db 192 aAlaProGlyValLeuArgGlnGlyAlaAlaGlyProAlaProProAlaArgSerPr 212
Qy 384 -----GGAGCGCGCAGCTTCCCAAT 403
Db 212 oArgArgAlaGlyGlyGlyIleGlnArgArgGlyArgLeuGlyAsnArgArgLeuProAl 232
Qy 404 TTGCGCCCCCTGAGGGCACCGCAGCTCATCCTTCTCTCTCTC-----GC 451
Db 232 aAlaAlaThrGlyGlnProArgArgGlyProHisTrpSerProValProArgAlaProAl 252
Qy 452 TCAGATGATTCACCGCTTCCACAACTCATCGACCGCTTGTCTGCTGA----- 500
Db 252 aAlaProAlaGlyAlaValProArgThrGlyGlyProGlyArgArgValLeuTyLeuHi 272
Qy 501 -----CCTGTC-----CCAAGCGCGCTGGTGGCGG 526
Db 272 sArgGlnProAlaAlaSerArgGlyValProGlyValGlnProArgArgProGly----- 290
Qy 527 TTGCGCGATCTTACGTGAGCGGCAAGTACACCTTCCCTCGC----- 569
Db 291 ---ArgGlnLeuArgProGlyAspAlaArgProAlaProGlyAlaGlyAspGlyAspArg 309
Qy 570 -----CCAGATGCCCTGGTGGCGCGCTTCTTCTTGGCGATCGATCT 610
Db 309 gArgGlnGlyAspArgHisProAspArgArgGluGlyLeuArgArgAlaArgAspAl 329
Qy 611 TCGACAT-----CGACCAACATTGACATCGGCGC-----CGAGCGCC 646
Db 329 aGlnArgProGlnProAspArgGlnArgGlnLeuArgProGlyGlyAlaArgArgArgPr 349

QY 647 GCGC-----CTACCTGGAGCAGAACTGGAGCGGTGGGAGCAGA 688
 Db 349 oArgArgGluProAlaArgAlaLeuProAlaAlaGlyGlnGly----ArgLeuGlyGlyAl 368
 QY 689 ACACCCA-----GGGTTT----- 701
 Db 368 aHisProArgProGlyGlnProAlaThrAlaGlyTyArgProAlaAlaAspAlaGlyG 388
 QY 702 -----GATCCCTTA-----CG 712
 Db 388 yAlaAlaAlaAspProLeuProArgArgLeuHisLeuPheArgThrGlyProArgGlnAr 408
 QY 713 TGCGGTG---GCTGGCGCCCTACTACGTGATGGCGCTGCCCGCCAGCGTGGCC 769
 Db 408 gAlaLeuGluAlaAlaAspAlaLeuArgArgLeuProHisArgArgProValPr 428
 QY 770 ACGCCCTGCACGAGCGCGTGA-----GCGCGCCGCCAT----- 806
 Db 428 oArgAlaGluProGlyLeuLeuGlyHisSerArgIleSerAsnAspAlaSerHisArgAr 448
 QY 807 -----GTTCCCGCCACCTTCCT-----GT 826
 Db 448 gSerLeuArgHisProGlyArgArgGlnArgLysProAlaArgProHisHisAs 468
 QY 827 ACAGCAGTCTGGGAGGACCCCGAGCGCGATATGA----- 863
 Db 468 pHisAlaAlaSerArgArgProArgProGlyThrGlyArgArgProProArgArgArgSe 488
 QY 864 -----GGTGATGAGATCAACCCCAAGCACCGGTGCTGACCCCTGACTAGCG 910
 Db 488 rLeuHisAlaAlaAlaAspGly---GlnPro-----GlyAlaAlaGluArgProAr 504
 QY 911 GCGGTGCAATGCCCTGAACCTGTGTGTCAGAGGGCGCGCAGGTGTGTCGTGGACT 970
 Db 504 gArgArg-----ProGlnProAlaGlyAlaGlyArgArgPro---ThrAlaGlyAspAl 521
 QY 971 GCACCCCGCCGAGTC-----GGCGCTTCGGAGCTGAAGAAGTGGCCATTCAGCAGC 1024
 Db 521 aHisProProAlaGlnHisHisArgProSerGlyAlaGlyGlnProAlaAlaThrAl 541
 QY 1025 TGGAGTTTGAGGAGCTGTGGCAGCTGTTTCGGCGAGGGCGT---GCACCCGCGCATTGAGG 1081
 Db 541 a-----ArgLeuProAlaProValArgGlyGluGlyThrProGlyArgArgGl 557
 QY 1082 AGCTGTACGAGAAGAGCTGGCGCCCTTCCTGTGCAAAACAGCA----- 1127
 Db 557 yAlaGlyArgSerAspAlaGlyAlaLeuArgAlaLeuHisArgProArgArgSerGlyAl 577
 QY 1128 -----CAACTTCGTGTCCAGCG---CCTCTGGTACTTCCAGC 1162
 Db 577 aGlnHisAlaValGlyGlnHisGlnArgLeuGlyGlnAlaGluProAlaAspHisProAl 597
 QY 1163 ACGGCTGTACTACGAGCGCGCATGGG----- 1190
 Db 597 aGlnArgGlyLeuGlyArgArgGluGlyLeuProValAlaArgThrLeuProAlaGluPr 617
 QY 1191 -----CAAGCTGTGGGTGTGTCAGTGCCT----- 1217
 Db 617 oAlaProAlaProAlaProAlaGlyAlaAlaValProValHisGlnProArgLeuArgAr 637
 QY 1218 -----GGCCGTGTGTGGGAC 1234
 Db 637 gProLeuProGlyHisAlaArgArgProGlnProThrGlyAlaAlaArgAlaHisAr 657
 QY 1235 TGGGCAAGACCGTCAAGCGCTCGCCCAACGCGCCCAATGGAGGAGCGCGCTGTGT 1294
 Db 657 gGlyGlyAspProGlnHisProArgArgValArgAlaArgThrValAlaAlaLeuAlaAr 677
 QY 1295 GGGACAGCAACATGCTCATCCA-----CTTCGTGA 1324
 Db 677 gProGlnArgAspAlaArgProProPheAlaAlaProAlaAlaValGlyArgTyArgHi 697
 QY 1325 AGAACGGGCCCCAGCGCTGGTGTGCTGTTTCGTCAAGTT----- 1364

Db 697 sArgProGlyLeuAlaAlaGlyLeuAlaValArgProAlaAspGluAlaGlyArgArgAr 717
 QY 1365 -----CGTGA 1369
 Db 717 gArgAlaGlyValGlnAlaHisProArgHisArgArgAspProGlyAlaGlyHisArgPr 737
 QY 1370 GCCTGGTGTCTTCAACAAGGC-----CGTCTGTGGTTCCGGCGCG 1411
 Db 737 oProGlyGlyAlaAlaAlaGlyAspArgAlaAlaThrProGlyAlaLeuProArgArgAr 757
 QY 1412 GCGTGCCTGGCGCAACA-----GTACGGCGCTGATCAAGCGCGACGCGCATCC 1456
 Db 757 gHisGlnGlyProAlaGlyGlyGlyArgArgProLeuGlyGlyArgHisPr 777
 QY 1457 CCA----- 1459
 Db 777 oArgArgArgAlaValArgGlnArgGlnArgAlaArgValProAlaAlaAl 797
 QY 1460 -----TT 1461
 Db 797 aAlaAlaHisArgArgArgProAlaGlnGlnGlyProGlyAlaGlyHisArgAlaAl 817
 QY 1462 GAGAACTACATCGCGCACCCATCGAGCGGTGGCGAGAACTCGCACGTGC----- 1513
 Db 817 eAlaThrThrGlyArgSerProArgCysAlaThrArgProThrGlyAsnCysProArgPr 837
 QY 1514 -GCAAGCAGAACTACTTCTACTCAACTGCTCAACCGCAAGTCTTCGCGGACAACTGC 1572
 Db 837 oAlaProArgArgSerProThrSerAlaArgProProAlaThrProAlaAlaSerPr 857
 QY 1573 CCCACCTACCTGCGCGAGG-----CGSCCTTCGCCACCTCAAGAGTGGCG- 1618
 Db 857 oProGlyAlaAlaThrProSerArgTyrArgProMetProAlaProLysAlaAlaHi 877
 QY 1619 -----TGGTGGACAACCT-----GACGCTCTCCACC 1644
 Db 877 sAlaThrAlaGlyTrp-LysSerProTyrSerArgArgAlaArgAsnGluArgLeuProG 897
 QY 1645 AACTTCTTCAT-----GGAGGAGCT----- 1664
 Db 897 lnLeuArgAlaLeuGlyGlyAlaGlyAlaArgProAlaArgProGluProAspHisL 917
 QY 1664 ----- 1664
 Db 917 euValProArgProAlaAlaAlaProGlyGlnLeuArgThrValGlyLeuGlyAspGlnP 937
 QY 1665 -----CAAAGCGCGCAC 1677
 Db 937 roLeuGlyAlaAspArgProAlaValProGlyLeuAspArgLeuProArgAlaAlaHis- 956
 QY 1678 TACACCAAGGTGATCTTGATGGACCACTGGCTGGTGGATATGCCGCTGCCCAACGAG 1737
 Db 957 --ArgAlaGlyProAlaGlnArgGlyGlyHisAlaGluSerArgArgGlyGlnArgA 976
 QY 1738 CTGSCCGA----- 1745
 Db 976 laGlyArgArgGlnArgArgHisArgArgArgAlaGlyAspProGlnAlaThrHisGlyA 996
 QY 1746 -----GTGCTGGCGCAAGCAGGTTGCGCGCGCGGCATCGT----- 1781
 Db 996 rGlyGlyProGlyProAlaGlnAlaGlyGlnAlaGlyArgGlnArgAlaAlaGlnProValA 1016
 QY 1782 -----CATCTGGCGCTCCGCTCCCTCAG----- 1805
 Db 1016 rgValAlaLeuValArgAspHisArgProAlaArgPheGlyGlnAspHisArgAlaAspG 1036
 QY 1806 -----CCGCCCTTA-----CGCCGAGCTGATCCAGAGGC- 1835
 Db 1036 luLeuArgProGlyLeuProAlaArgArgThrAspGlyArgArgGlyAspProArgGlyA 1056
 QY 1836 -----GGCCTTCGAGCTGGCTGCATCCCGCGCCACTCAGGCTACATGAC 1884

Db 1056 rgArgHisAlaGlnLeuArgLeuValValHis-----ArgArgSerGlyAlaAlaGlyH 1074
QY 1885 CGCGTCAACATGTACAGCTCTTTCATATGCGCCCGCGAAGGCGCCCAAGAGACAA 1943
Db 1074 lsArgArgPro-----LeuTyrHisProGlyGlnProArgProGlyGlyGln 1089
RESULT 7
US-09-252-991A-27068
; Sequence 27068, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27068
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27068

Alignment Scores:
Pred. No.: 1,39e-15 Length: 638
Score: 223.00 Matches: 194
Percent Similarity: 32.6% Conservative: 36
Best Local Similarity: 27.5% Mismatches: 239
Query Match: 8.9% Indels: 236
DB: 2 Gaps: 38

US-10-620-914-44 (1-1947) x US-09-252-991A-27068 (1-638)

QY 1939 CTTCTTGGCGCCCTTCGCGCGGCCATGTAGAAGAGCTGTACATGTGTGACGCGGTCCA 1880
Db 66 ProArgGlnArgArgArgAlaProAlaGlyArgAlaAlaSer-----Pro 81
QY 1879 TGTAGCCCTGAGTGGCGCGCGGATGACGCGCAGCTCGAAGCCCG----- 1835
Db 82 GlyLysProArg-----ArgGlyLeuAlaGlyAlaThrAlaGlyProArgProArg 100
QY 1834 -----CCTTCTGGATCAGCTCGG-----CGTAGGCGGCTGAGGAGCGGAGCGCC 1787
Db 101 AlalysProArgGlyValAlaArgIleGlnArgArgProAlaArgArgGlnAla 120
QY 1786 AGATGACGATCGCGCGCGCAACCTCTTGGCCAGGC---ACTGCGCCAGCTCGTTGG 1730
Db 121 -----ArgArgProAlaGlyProAlaAlaThrGlyArgAlaArgProHisArgGln 138
QY 1729 CCACGGGCA----- 1721
Db 139 ProGlyThrMetValArgLeuProGlyArgArgGlyGlyAlaAlaProGlyArgArgLeu 158
QY 1720 ---TATCCAGCCAGTCCACAGTGGTCCATCAGAAATCACCTTGGTGTAGTGGCGGCTTGA 1664
Db 159 ProHisProAlaAlaAlaArgGlnProAlaProArgPro----- 171
QY 1663 GCTCTTCCATGAAGAAGTTGGTGAGACGGTCAGGTTGTCCA-----CCACGCCAC 1613
Db 172 -----ProGlnProGlyProArgGln 178
QY 1612 TCTTGAAGGTGCGNAGCCCGCTCGCCAGTAGTGGGCGAGTTGTCCGCGAGGA--- 1556
Db 179 Ala---GlyGlyArgGlnProGlyProGlyArgArgArgAlaArgAlaGlyGln 197
QY 1555 ACTTCCGCTGAGCGAGTTGTAGTAGAGTAGTCTGCTTGGCAGCGTGCAGTCTCCG 1496
Db 198 ProAlaArgAlaGlyArgAlaAspArgGlyLeuAlaAlaAlaArgArgAla----- 214

QY 1495 CCACGCGCTCCATGGTGC CGCGATGTAGTTCTCAATGGGATGCCGTC CGCTTGTATCA 1436
Db 215 ---ArgArgAlaThrLeuGlyGlnArgArgLeuArg----- 225
QY 1435 GCGGCTACTGCTTCCCGGCACGCGCGCGCGAACCACAGCACGCGCTTGTGAAGACA 1376
Db 226 ---ArgHisAspGlyAlaGlyArgArgArgGlyTTPaArgGlnCnArgArgPro 244
QY 1375 CCAGGCTCACGAATCTTGACGAACACAGCACGCGGCTTGGGCGCTTCTTCACGAAGT 1316
Db 245 ArgArgGlyAlaAlaAlaArgThrArgGlnProAlaAla---ThrLeuSerGlyArg--- 262
QY 1315 GGATGAGCATGTGCTGCTCCACAGACGCGCTGCTCTCCATTTGTGGGCGGTGGCGA 1256
Db 262 ----- 262
QY 1255 GCGCTTGACCGTCTTCCCGAGTCCCGACACAGCGCGCAGGCACTGACAGCCAGCACA 1196
Db 263 -----ValAlaProHisProArgProAspArgAlaSerProAlaThr 276
QY 1195 GCTTGGCCCATCGCGCTGTGTACAGCGCTGTGAAGTACCAGAGGCGCTTGGACC 1136
Db 277 ValArgArgHisArg---ArgGlnThrGlyArgGly----- 287
QY 1135 AGAAGTTGTGGTGTGTCGACAGGAAGGCGCAGCTTCTTCTGTACAGCTCTCTCAA 1076
Db 288 -----AlaProGlyProGlyHis-----ProGly 295
QY 1075 TGC GGGGTGCACGCCCTCGCGCAACAGCTGCCACAGCTCTCAAACTCCAGCTGCTGAA 1016
Db 296 ThrAlaGlyAlaArg---ArgThrProAlaProAlaArgProGlyThrProAspProGly 314
QY 1015 TGGCCACCTTCTTCAGCTCCAGAAAGCGCCDAGCTCGCGGGGTTGCGAGTCCACCCAGACA 956
Db 315 TrpAspAspArgProAspPro---AlaHisArgProArgHisArgGlnProAlaAlaThr 333
QY 955 CTTGGCGCGCCCTTCGACACAGCAGTTTCAAGGCAATTCAGCAGC---CGCGCTAGTTCAGGG 899
Db 334 ProGlyAlaGlyProArgAlaThrGlyAlaGlyAlaLeuGlyLeuGlyArgArgArgLeu 353
QY 898 TCAGCAGCTGCTCTTGGGTTGATCTCCATCCTCATATCCGCTCGGGGCTCTCC 839
Db 354 LeuAlaPro-----HisIleProAlaTyrProHisArgGlyPro--- 366
QY 838 ACAGCTGCTGTACAGAAAGTGGCGGGAACATGCGCGCGCTCCACAGCGCTCTCGT 779
Db 367 -----AlaGlnProGlyArgPheAlaGluProProAlaGlnLeuProArg-----Arg 382
QY 778 GCAGGCGGT-----GGCAACGCTGGGAGGCGGCAATCC 743
Db 383 AlaGlyArgArgAspProProArgArgThrGlyArgArg-----GlnGlnPro 399
QY 742 ACAGTAGTAGGGGCGCGCAGCCACGCGCAGTAGGGATCGAACCTTGGGTGTTCTGCT 683
Db 400 AspProGlyArgGlyGlnGlnArgProAlaArgArgGlyArgAlaProGly-----Arg 417
QY 682 CCCACAGCGCTCCAGCTTCTGCTCCAGGTAGGCGCGCGCTCGGGGCGGATGTCAATGT 623
Db 418 ArgTyrArgAlaAspProArgArgProArgArgHisGlySerGlyAsp-----ProAla 435
QY 622 TGTGATGTGGAAGATCGATCGCAGAAAGAACCGCGCGCAGCCAGGCGATCTGGGCGAGGG 563
Db 436 GlyArgArgArgGlnProAspArgArgArgGlnSerGlnArgArgProGlySerGly 455
QY 562 GCA-----GGTCTACTTCCCGCTCA-----CGTAGA 536
Db 456 AlaTrpProAlaGlyAspArgArgGluProGlyArgProAlaArgAlaGlyArgArgGly 475
QY 535 AGTCGCAACGCCACCCAGCGCTTGGGACAGGTACGACAGGCTGCTGCTGATGACGT 476
Db 476 AlaArgGlnArgProValAspArg-----AlaProGlyArg----- 487

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QY 475 TGTGAAACGGTGAATCATCTGTCGAGCGAGTAGGAGAGGTCATGAGCGTCGCGGTGCCCT 416
Db 487 -----
QY 415 CAGGGGGCGCAATATGTCGAACGCTGGCCCTCCACGACCTGGACATCTTCCAGCCCTTGG 356
Db 488 -----GlyValGlyAspHisArg-----
QY 355 CCTTCGCCCTTCTTCTGGCCACCTCGCACAGCGAGTGGCCACAGGTTCGACACGTCAGATGG 296
Db 494 -----GlnArgAlaAspGlyAspProLeuAspArg-----
QY 295 ACTTGAACCTCCGACGAGTCGATGTAATCAGCCATCATATCGACATCTCCCGCAGTGGCCAC 236
Db 504 -----ArgThrAspGlnProAla-----
QY 235 CACCCAGGTCAACCCAGATGAGTTCGAGCGCTCGGCCAGCGGGCGAG---CAAAGGCGAG 179
Db 515 HisArgGlyArgProArg-----ArgArgProGlyProArgLeuArgArgGly 530
QY 178 CGGCTGGGGCCGTAGAACCTCTCCAGCGAGCAGCGTCGATCGC----- 131
Db 531 ArgArgGlySerProLeuAlaGlyProAlaHisArgArgHisArgGlyAspProAla 550
QY 130 -----CCTCTCTGTCGCGAACCCACATATGTCGCGAGAACGGTCAAGTCATCCT 83
Db 551 AlaHisArgProProAlaThrGlyArgAlaAlaGlyGlyHisAlaGlnProGly 570
QY 82 TCATGCTGCTGAGCTTGAGCTTCTCCAGGGAGAGTCTTCTTGGTGTGAGCTCGAGGCC 23
Db 571 ArgAlaCysArgThrHisArgArgThrGlyArgArgGlyGlyArgArgAlaGlyArgSer 590
QY 22 GCGCGTCACGACCCG 8
Db 591 GlyArgArgAspPro 595

RESULT 8
US-09-252-991A-18296
; Sequence 18296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18296
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18296

Alignment Scores:
Pred. No.: 3.14e-15 Length: 467
Score: 317.50 Matches: 178
Percent Similarity: 32.7% Conservative: 26
Best Local Similarity: 28.5% Mismatches: 198
Query Match: 8.8% Indels: 222
DB: 2 Gaps: 34

US-10-620-914-44 (1-1947) x US-09-252-991A-18296 (1-467)
QY 1828 GGATCAGTTCGGCTAGCGGGCTGAGGAGCGGAGCGGCAGATGACGATGCCGCCG 1769
Db 3 GlyCysAlaGlyCysProAlaGlyCysGlyArgArgGly----- 15
QY 1768 GCGCAACCTGTTGGCCAGGCACTCGGCGAGTCTGTTGGCCACGCGGCATATCCAGCAGT 1709

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Db 16 -----AsnTrpProProAlaArgAlaGlyPheProProPro-----ProAlaCys 31
QY 1708 CCAGTGGTTCATCAGAAATCACCTTGTGTAGTGGCGGCTTTGAGCTCTCCATGAAGA 1649
Db 32 ArgProGlyThrGlySerSerArgTrpAsnArgAlaGly----- 44
QY 1648 AGTTGGTGGAGACGGTCAGGTTGTCCACACCGCCACTCTTGTAGGGTGGCGAAGGCCGCT 1589
Db 45 -----ArgAlaArgGlyCysPro-----GlyCysAlaAlaProPro 56
QY 1588 CGC-----GCAGGTAGTGGGGCGAGTGTTCGCGAGGAACCTTCCGGTGGAGGC 1541
Db 57 AlaGlyValProGlyAlaGlyArg-----SerValProAlaProAlaCysArg----- 72
QY 1540 AGTTGTAGTAGAAGTAGTCTTCGTCGCGACGTCCGAGTCTTCGCCACGCCGCTCCATGG 1481
Db 73 -----ArgArgArgHisArgArgSerArgProSer-----GlyArgProArg 88
QY 1480 TGGCGCGATGTAGTCTCAATGGGATCGCTCGGCTTGCATCAGCGCGTACTGCTTGC 1421
Db 89 GlnGlyArgArgGlySer-----ProThrAlaAlaLeuArgLeuArg 102
QY 1420 CCGCAGCGCCGCCCGCAACCCACAGCAGCGCTTGTTCAGAGGAGCCAGCGGTCTCAGAACT 1361
Db 103 ProAlaArgArgArg-----ArgHisPro----- 111
QY 1360 TGACGAACAGCCACACAGCGGCTTGGCCCGTCTTCACGAAGTGGATGAGCATGTTC 1301
Db 112 -----AlaTrpArgArgArgSerAlaSerArgProAla----- 122
QY 1300 TGTCCACAGACGCGCTGCTCTCCATTGTGGCGCGTTCGCGAGGCGCTTGACGGTCT 1241
Db 123 -----GlyAlaProPro----- 127
QY 1240 TGCCAGTTCACAGCAGCCAGCGCTTGCAGCACCAGC----- 1199
Db 128 AlaProCysProAlaProArg--GlyAlaGlyAlaProSerValArgGluArgProAla 146
QY 1198 ---ACAGTTGCCATGCCGCCCTGGT-----AGTACAGGC 1166
Db 147 GlySerAlaProProArgProAlaArgArgProProAlaProHisArgThrGly 166
QY 1165 CGTCTCGAAGTACCAGAGCGCTTGGACCAAGTGTGGCTGTGGTTGCGACAGGAAG 1106
Db 167 GlySerGly-----TrpArgArgArgGly-----ArgThrArg 178
QY 1105 GCGCAGCTTCTTCTCGT-----ACAGCTCTCAATGCGCGGTGCACGC 1061
Db 179 ArgProAlaAlaSerArgArgProAlaGlyGlyProAlaGlyArgProGlyGlySerArg 198
QY 1060 CCTGCGCAACAGCTGCCACAGCTCCTCAACTCCAGTGTGTAATGCCACCTTCTTCA 1001
Db 199 AsnArgArgArgAla----- 203
QY 1000 GCTCCAGAAAGCGCGACTGTCGCGGGTTGCAGTCCACCGACACCACTTGGCGGCCCT 941
Db 204 -----GlyCysArgProAlaArgProValAlaArgAla 215
QY 940 GCACAGCAGGTTTCAGGCAATTGAGCGCGCTAGTCAGGGTCAGCACCGTGTCTTGG 881
Db 216 GlyPro--GlyProGlyArgCysArgArgArgCysAlaTrpSerProCysPro--- 233
QY 880 GTTGATCTCCATCACCTCCATATCCGGCTCGGGGTCTCCACGACTCGCTGTGTACAGGA 821
Db 233 ----- 233
QY 820 AGTGGGGCGGAACATGGCGCGCTCCACGCGTCTCTGAGGGCGGTGGCCAAAGC 761
Db 234 -----ThrProArg--AspArgAlaGlyAlaGlyAspArg 244
QY 760 TGGGACGGCGGCCAATCCACAGCTAGTAGGGGG-----CGCGCAGCAGCCGACGT 710

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Db 245 HisValProAlaGlyAspAlaArgAlaAlaGlyTrpProThrGlySerArgCysAlaArg 264
QY 709 AGGGGATCAACCCCTGGGTCTCTGCTCCACACAGCGCTCCAGCTCTGCTCCAGGTAGG 650
Db 265 ArgSerGlySerAlaGlyCysAlaArgPro-----ProArgArgSerCysValArg 281
QY 649 CGCGCGCTCGGGCCGATGTCATGTTGTGCGATGTCGAAGATCGATCCGCAAGAAGAAC 590
Db 282 TrpAlaAlaArg-----ArgValAlaAlaArgAspSerAlaArgArgSer 295
QY 589 GCGCGACACAGGGCATCTGGCGCAGCGGCGAGGTCTACTTGGCGGTCCAGTAGAAGTGG 530
Db 296 AspArgProValArgSerAlaLeuArgGlyLeuProAlaAlaArgArgSerArgProArg 315
QY 529 CAACGCCACACAGCGCTTTGGGACAGTACGACCAAGCCCTGTCGATGACGTTGTGGA 470
Db 316 HisArgArgProGlySer-ValProProValArgThrSerArgAla-----ThrProAr 333
QY 469 ACGTGGGAATCATCTG-----GAGCGAGTAGAGAGAGGTGATGACGTCG 425
Db 333 GArgTrpHisAlaArgTrpGlnAlaAlaAlaArgProGly-SerValLeuSerSerA 353
QY 424 CGGTGCCCTCA-----GGGGCGCAAAATTGGCAAGCGTCGGCCCTCCACGA 380
Db 353 laThrProAlaAlaProGlyValArgGlyTyProArgGluTyAla-ArgAlaProArg 372
QY 379 CTTGACATCTTCCAGCCCT-----TGGCCCTTCCCTCTTCTTTGGCCA 335
Db 373 ProAlaLeuProGlyArgProAlaAlaAlaArgProAlaArgProArgProCysArgArgPro 392
QY 334 CTGCGCACAGGAGTGGCACAGGTGCGACCA-----CGTAGATGGACT 293
Db 393 AlaAspArgSerProGlyGlnGlyArgProProGlySerSerAlaThrArgArgTrpArg 412
QY 292 TGAATCTCGCCAGTCGATGTAATCAGCCATCATATCAGCATCTCTCCACGTCACCCAC 233
Db 413 -----ProCysHisArg 416
QY 232 CCAGGTCAACCCAGATAGGTTTCAGCGCTCGGCCAGGC-----GGGCAG 188
Db 417 ArgAlaGluProAlaAlaAlaProAlaGlyTyProGlyAlaAlaAlaArgSerAlaThr 436
QY 187 CAAGGCGAGCGCTGGGGCCGCTAGAAC-----TCTCCAGGCGAGCAGCGTATCATGCG 131
Db 437 ArgArgThrHisAlaGlyArgArgGlySerAlaThrProSerGlyArgArgAspArgArg 456
QY 130 CTTTCT 125
Db 457 ProAla 458

RESULT 9

US-09-252-991A-31760
; Sequence 31760, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31760
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760

Alignment Scores:

Pred. No.: 6.27e-15 Length: 1706
Score: 316.50 Matches: 193
Percent Similarity: 33.1% Conservative: 44
Best Local Similarity: 26.9% Mismatches: 249
Query Match: 8.7% Indels: 231
DB: 2 Gaps: 36
US-10-620-914-44 (1-1947) x US-09-252-991A-31760 (1-1706)
QY 1846 CGTCAAGCCCGCTTCTGGATCAGCTCGGCTAGGCGGCTGAGGAGCGGAGCGCC 1787
Db 276 ArgArgGlnProAlaGlyAlaThrAlaArgLeuArgHisArgProGly---HisProAla 294
QY 1786 AGATGACGATCGCCCGCGCAACCTCTTGGCCAGGACCTCGGCCAGCTCGTTGGGCCA 1727
Db 295 ArgLeuArgArgGlnProAlaArgLeuArgSerGlyGluArgProAlaGluSerPro 314
QY 1726 CGGGCATATCCAGCCAGCTCCACGTGGT----- 1700
Db 315 ArgArgThrProGlyGluLeuArgGlyArgArgProAspAlaLeuProArgLeuAlaGly 334
QY 1699 ---CCATCAGAATCACCT-----TGGTGTAGGTGCGGCTTTGAGCTCCT---CCATGA 1652
Db 335 LysProGlyArgTyProAlaGluPheAlaArgGlyAlaAlaProAlaProGlyPro--- 353
QY 1651 AGAAGTTGGTGAGACCGGTTCAGTTGTCACCCAGCCACTCTTGAGGG-----TGG 1601
Db 354 -----LeuAlaAlaAlaValProArgArgHisAlaAlaArgAlaAlaGluProTrp 369
QY 1600 CGAAGCGCGCTCCGCGAGGTAGTGGGGAGTGTCCGCGAGGACTTGGCGGTGAGGC 1541
Db 370 ArgArgProAlaGlyGlyArg-----AlaAspArgThrAlaThr----- 383
QY 1540 AGTTGTAGTAGAAGTAGTTCTGCTTGGCAGCTGCGAGTTCTCCGCCACGCGCTCCATGG 1481
Db 384 AlaProAlaArgProArgThrAlaCysAlaAlaAlaValAlaGlyProArgHis----- 401
QY 1480 TGC CGCGATGATGTTCTCAATGGGATGCGCTCGCTTGTATCAGCGCGTACTGCTTGC 1421
Db 401 ----- 401
QY 1420 CCGGACGCGCGCCCGNACCAGCAGCGGCTTGTGAAGAGCAGCAGGCTCAGCA--- 1364
Db 402 ---AlaArgGluGlnProArgThrLeuProGlyProArgProGlyProGlyAlaAlaGly 420
QY 1363 -----ACTTGACGAACAGCCACAGCGGCTTGGCGCCGCTTCTTCACGA 1319
Db 421 ThrHisLeuAlaGlySerAlaGlnProAlaAlaProAlaAla---AlaArgProPro--- 438
QY 1318 AGTGGATGAGCATGTTGCTGCCACAGCGCGCTGCTCTCCATTTGTCGCGCGCTTGG 1259
Db 439 -----AlaAlaLeuProAlaAlaArgAlaArg--- 446
QY 1258 CGAGCGCTTGACGCTTGTGCCAGTCCAGCACCA-----CGGCCAGGCACTGCA 1208
Db 447 ArgGlyArgArgGlnProProGlyArgProProArgArgLeuArgProGly---Ala 465
QY 1207 GCACCCAGCAGCAGCTTCCCATCGCGCTGTTAGTACAGGCGCTGTGGAAGTACCAGA 1148
Db 466 ProValAlaAlaAlaPro-----AlaThrGlyGlyAlaAlaThrGluPro 481
QY 1147 GCGCCTTGGACAGAGTGTGGCTGTTGCGACAGAGGCGGCCAGCTCTTCTCTCGT 1088
Db 482 GlyAla-----GlyAspSerArgHisArgCysArg 491
QY 1087 ACAGCTCTCATCGCGGGTGCAGCGCTCGCGAACAGCTGCCACAGCTCTCTCAACT 1028
Db 492 SerGlyThrAspArgProGly---ArgProArgGlnProAlaAlaAlaArgAspProGly 510
QY 1027 CCAGCTGCTGAATGCCACCTTCTTACAGTCCAGAGCGCGCAGCTGCGCGGGTTCAGT 968
Db 511 ProGlySer---TrpProGlyProSerAlaAlaAlaArgAlaAlaArgArgGly---Asp 528

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QY 967 CCA-----CCGACA 959
Db 529 ProHisArgArgGluThrAlaLeuArgSerAlaAlaArgArgProArgArgAlaAsp 548
QY 958 CCACCTGGCGGCCCTTCACACAGCAGGTTTCAGGGCATTGCAGCCGCCGTAGTCAGG 899
Db 549 ProProGlyArgThrProAlaGlnProGlyGlnThrGluGlyAlaArg- 565
QY 898 TCAGCACGCTCTCTGGGGTTGATCTCCATCATCCTCCATATCCGGCTCGGGTCTCTCCC 839
Db 565 ----- 565
QY 838 ACGACTGCGTGTACAGGAAGTGGCGGAACATGGCGCGCTCCACGCGCTCTCGT 779
Db 566 -----LeuAlaArgArgThrAlaGlyThr-----AlaAlaProArg 578
QY 778 GCAGGGCGTGGCCCAACGCTGGCGAGCGGCCAATCCACACGTAGTAGGGCGCGCGACCC 719
Db 579 HisArgArgGlnProGluGlnProAlaGlyProArgProProAlaArgGlyAlaThrAla 598
QY 718 ACGCACGT-----AGGGATCGAACCTGGG 692
Db 599 ThrSerArgLeuProAlaLeuProTrpProArgArgProAlaArgSerHisArgProGly 618
QY 691 TGTTCGTCTCCACACGCGCTCCAGCTTCTGCTCCAGGTAGCGCGGCTCGGGCCGA 632
Db 619 IleProGlyProAla---AlaProAlaProGlyThrThrArgArgAspSerArgArgArg 637
QY 631 TGTCAATGTTGATGTCGAAGATCGATCGCCAGAGAAACGGCGCGCACCGGCA--- 575
Db 638 -----ThrArgSerHisGlyAlaProHisAlaGln 647
QY 574 -----TCTGGCGCAGGGGAGGTGCTACTTCCGCTCACGTAGTAGTCGGCAAGC--- 524
Db 648 ProArgSerAlaAlaGlyLeuGluAlaAlaProGlyThrArgGlnSerGlyThrAlaVal 667
QY 523 CCACGAGCGCTCTTGGACAGGTACGAGCAAGCTGCTGCATGACGTGTGGAACGGTG 464
Db 668 GlnProGlyArgSerGlnGlyGlnGlyArgGlnProArgArgSerArgGlyCysAlaAspAla 687
QY 463 GAATCATGTCGAGGAGTGGAGAGGTGATGAGCGTCGCGTGCCCT---CAGGGGCGC 407
Db 688 ArgAlaGluProArgThrAlaArgGlnGlyHisArgArgAlaProGlyGlnProGln 707
QY 406 CAATTGGCAGCGTCGCGCTCCAGCACCTGGACATTTCTCCAGCCCTTGGCCCTTCGCCT 347
Db 708 AlaMetGlyArgArgHisProPro-----AspArgGln 718
QY 346 TCTTCTTGGCCACCTCGCACAGCGAGTGGCACAGCTCGACCGTCCAGCCAGTGTGAAC 287
Db 719 AlaLeuAlaAlaProAlaArgValHisArgAlaGlyArgArgThrArgProAspGluPro 738
QY 286 TCGCCAGGTGATGTAATCAGCCATCATATCGACATTTCTCCAGTGTCCACACCCAGGT 227
Db 739 AlaProGlyLeuAlaAspGluPro-----ArgProGly 749
QY 226 CAACCCAGATGAGTTCGAGCGCTCGGCCA----- 197
Db 750 GlnProArgAlaAlaAlaGlnGlyArgAlaValArgHisGlyAspLeuArgArgSerLeu 769
QY 196 -----GGCGGGCAG 188
Db 770 AlaAspAlaGlyGlyValArgProAlaAspProLeuSerArgAlaGlyHisGlyGlyGln 789
QY 187 CAAGG-----CAGCGCCTTGGGCCCGGTAGA 161
Db 790 ArgArgArgGluAlaAspAlaAlaAspArgValLeuLeuGlnProArgGlyLysArgArg 809
QY 160 AGCTCTCAGCGGACGCGTATCATCGCCTTCTTCTGCTCCGACACCATATGGCGCA 101
Db 810 GlyArgThrValArgArgArgSerAlaArgArgGlyArgArgArg-----GlyAla 826
QY 100 GAACGGTCA-----GGTCATCTTCATGCTGCTGAGCTTGAGCTTCTCCAGGAGAAAGT 47
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Db 827 AlaArgSerLeuArgGlyHisLeuGluProProArgAspGlnGlyLeuProGlyProPro 846
QY 46 TCTTCTTGGTGTAGCTCGAGCGCGCGGTAC-----GACCGACCCCA 2
Db 847 AlaThrGlyAlaGlnArgProAlaGlnHisHisProAlaAspProLeuPro 863
RESULT 10
US-09-252-991A-27341
; Sequence 27341, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27341
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (803)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-27341
Alignment Scores:
Pred. No.: 1,58e-14 Length: 1073
Score: 310.00 Matches: 243
Percent Similarity: 28.1% Conservative: 41
Best Local Similarity: 24.0% Mismatches: 288
Query Match: 8.6% Indels: 440
DB: 2 Gaps: 47
US-10-620-914-44 (1-1947) x US-09-252-991A-27341 (1-1073)
QY 18 CGCGCGCGCTCGAGCTACAC-----CAAGAAGAACTTCTCCCTGGAGAACTCAA 68
Db 92 ArgCysSerCysThrLeuGlyAlaSerIleArgGluGluArgGlnProAspGluArgLys 111
QY 69 GCTCAGCAGCATGAAGGATGACCTGACCGTTCTCGCCCATATGTTGTTCCGCGACGAAGA 128
Db 112 AsnAlaArgHis-----ValProProArgArg 120
QY 129 GGGCGATGATCACGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGCGCGCTGCTTTCG 188
Db 121 ArgArgProGlyProCysArgProGlyProLeuHisAlaArgLeuProArgValArgArg 140
QY 189 TGCCCGCTGGCGCGCGCTCGAACCTCATCTGGGTTGACCTGCTGGTGTGCTGCTGGGA 248
Db 141 ProProArgGlnArgLeuAlaGlu----- 148
QY 249 GAATGTCGATATGATGGCTGATTACATGACCTCGCGAAGTTCAAGTCCATCTACGTGCT 308
Db 149 -----HisArgArgArgArgArgLeuTyLeuArgHis 160
QY 309 CGACCTGTGCCACTCGCTGCTCGAGGTGGCCCAAGAA----- 344
Db 161 ArgArgGlnProLeuProArgArgGlyGlyHisValValHisGlnHisArgProGly 180
QY 345 -----GAAGCGAAGCGCAGGGCTGCAAGAAATGTCACAGT----- 380
Db 181 AlaArgGlyAsnGlySerHisArgGlyArgAlaAspProProAlaGlyLeuPheGlnSer 200
QY 381 -----CGTGGAGGC 389
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Db 201 LeuLeuArgHisGlyGlnProAlaArgHisArgThrLeuProGlnAlaArgAlaGly 220
QY 390 CGACCTTGGCCAAATTTGGCCGCC-----TGAGGG 419
Db 221 ProArgPro-----ArgProArgValProHisHisArgArgPheHisArgGly 238
QY 420 CACCGGAGCTCATCACCTTCTCTCA----- 446
Db 239 HisArgAspProProHisAlaLeuLeuProGluLeuProArgGlnAlaArgGlnGluAla 258
QY 447 CTCGCTCAGATGATTCACCGTTCCA----- 473
Db 259 ArgHisHisAlaAspGlnArgLeuProArgLeuAspLeuProArgHisValAlaGlyArg 278
QY 474 CAACGTCATCGACCA----- 488
Db 279 GlnGluArgArgProAlaGlyArgValArgLeuProArgAlaHisProProCys 298
QY 489 ---GGCTTCTCGTACCT-----GTCCCAAGCGGCT 518
Db 299 LeuSerLeuLeuLeuProArgSerGlyArgSerGlyArgGlyArgValProArgTrpPro 318
QY 519 GGTGGCGCTGCGGACTT----- 536
Db 319 GlyGlyGlyValArgThrGlnAspProArgThrGlyArgArgProGlyGlyGlyValHis 338
QY 537 -----CTAGCTGAGCGGCAAGTACGACCTGCCCTCGCCA 572
Db 339 LeuArgAlaGlyValArgLeuArgArgAspArgProAlaArgGlyLeuProProAla 358
QY 573 GATGCCCTGTGGCGCGCTTCTT---CTGGGATCGATCTTGGACATCGACAATTGA 629
Db 359 AspValGlySerValProAlaLeuArgAlaValHisLeuArgArgSerGlyAspLeu 378
QY 630 CATGGGCCCGGAGCCCG----- 647
Db 379 LeuArgProProArgProLeuLeuArgGlnProGlyGlyValArgArgThrAlaGlyHis 398
QY 648 -----CGCTTACCTGGAGCA----- 662
Db 399 HisProHisArgGlnGlyProHisLeuArgLeuProAlaAlaGlyArgValHisLeuLeu 418
QY 662 ----- 662
Db 419 ProAlaHisLeuGlyAspArgAlaGlyGlnGlyProLeuLeuGlnProTrpPhe 438
QY 663 -----GAAGCTGGAGCGGTGGGAGCAGACACCCAGGGTTCGATCCC 707
Db 439 HisLeuLeuArgProProGlyGlyLeuArgGlyGlyAlaGluHisArgAspHisArg 458
QY 708 CTAGCTGCGTGGCT-----GCGCGCCCTTACTACGTGTGGATTTGGCCG 752
Db 459 AlaArgGlyLeuAlaArgProArgArgArgGlyArgProLeuLeuArg-----GlyAla 476
QY 753 CTGCCCCAGGTGGCCACGCCCTGCA----- 779
Db 477 ProAlaLysSer---ProArgProAlaHisArgArgArgAlaArgAspAlaLeuHis 495
QY 780 -----CGAGGAGCGGTGGAGCGGCCCATCTTTCCTCCGCC 815
Db 496 GlyLeuCysArgValArgArgGlnGlyGlnGlyAlaValSerGlyLysProGlu 515
QY 816 CACCTTCTGTACAGCAGTGTGGGAGGACCCGAGCGGATAT-----GGA 863
Db 516 HisArgArgVal-----GlyProProAlaGlyAlaGluAlaArgProAla 530
QY 864 GGTGATGAGATCAACCCAGGACAC-----GTTGCTGACCTTACGTAGCGCGG 914
Db 531 GlySerSerAspArgProProGluArgAspValAlaAlaAspProHisProArgThr 550
QY 915 CTGCATCCCTGAACCTGCTGGTCAGGGCGGCCGAGTGTGTGCTGGTGGACTGCA 974
Db 551 GlyArgTyrArgGlyProGlyAlaAlaArgGluHisArgGlyAsnArgGlyGlySerCys 570

QY 975 CCCCGCGCAGTCGGCGCTTCT---GGAGCTGAAGAAGGTGCCCATTCAGCAGCTGGAGTT 1031
Db 571 ProArgArgSerProValSerAlaGlyAlaProProAlaProHisProAsnIleGlnGlu 590
QY 1032 TGAGGACGTGTGGCAGCTGTTTCGGGAGGdGCTGCACCCGCGCATTTGAGGAGCTTACGA 1091
Db 591 AsnProAsnGlyArgGlnGlnGlnGlyProAlaValAlaArgCysGlyAlaLeuHis 610
QY 1092 GAAGAAGCTGGCGCTTCTGTCGCAACACGACCACTTCTGTCGAAGCGCTCTG 1151
Db 611 GlyLeuGlyAspAlaLeuHisGlyProAspArgProGlyPheLeuProArgSer----- 628
QY 1152 GTACTTCCAGCAGCGCTGTACTTACAGGGCGCATGGCAAGCTGTCTGGTCTGCA 1211
Db 629 -----ValGluProValLeuValAlaLeuArgAla-----GlyProAla 641
QY 1212 GTGCTGCGCCCTGCT-----CCTGGGACTGGGCAAGACCGTCA----- 1250
Db 642 ValProAlaAspGlyHisAspAspLeuArgAlaGlyHisArgLeuProArgGlnArg 661
QY 1251 -----GCGCTCGCCCAACGCGCCCAATGAGGAGCAGCGCGCTCTGTG 1295
Db 662 ArgLeuProLeuGlyAlaGlnArgLeuArgLeuProLeuGlyGly-----ProGlyVal 679
QY 1296 -----GGACAGCAACATGCT-----CATCCATCTCGTGAA 1325
Db 680 MetAspValLeuGlyGlnArgThrValAspAlaPheGlyLeuHisProValArgGln 699
QY 1326 GAA-----CGGCCCCAAGCCGCTGTGTGGCTGTTCGTCAGTT 1364
Db 700 HisAlaArgArgLeuLeuPheProArgAlaGluProLeuGly---GlnAspArgHisArg 718
QY 1365 CGTGAGCTGTGTGCT-----CTTCAACAAGCCGCTGCT----- 1397
Db 719 HisSerProGlyAlaAlaHisArgGlyValGlnArgGlyArgAlaAlaProGlyGlnVal 738
QY 1398 GTGTTTCGGCGCGCTGCGGCAAGCAGTACGC---GCTGATCAAGGCGGAGCGCAT 1454
Db 739 AlaAlaGluProArgAlaAlaGlnAlaAlaArgGlyAlaArgProGlyArgArg 758
QY 1455 CCC-----CATTGAGAACTACATCGCGG 1478
Db 759 ProAlaLeuArgLeuGluProTrpLeuArgGlnArgLeuGlnProGlyLeuHisArgPro 778
QY 1479 -----CACCATGGACGGCT 1493
Db 779 ValLeuAlaGlyProAspGlyArgAlaGlySerAspGlyLeuTrpHisHisGlyAspArg 798
QY 1494 GCGGAGAACTCGCACCGTCGCAAGCAGAACTACTTCTTACAACTCGCTCACCGCAA 1553
Db 799 AlaGlyLeuLeu***-----ArgArg 805
QY 1554 GTTCTTGGCGCAACTGCCCCCCTACTTCTGCGGAGGCGG----- 1595
Db 806 GlyTyrAlaGlnArgAlaProArgHisProAlaArgGlyGlyAspLeuArgAlaAspArg 825
QY 1596 -----CTTCGCGCACCTCAAGAG---TGGCGTGGT---GGAACAACCTGAC 1634
Db 826 ArgArgLeuGlnHisLeuArgHisProArgArgAlaGlyArgGlyThrGlyArgGlyAsn 845
QY 1635 CGTCTCCAC----- 1643
Db 846 ArgArgHisProAspLeuArgProTrpLeuGlnHisLeuArgProArgArgArg 865
QY 1644 -----CAACTCTTTCATGGAGGACT 1664
Db 866 ArgAspAlaArgArgProGlyArgArgLeuArgProValHisProLeuHisGlnHisGly 885
QY 1665 CAAAGCGCGCACCTACACCAA-----GTTGATTCTGTGACCACTGAGTGGACTG 1712
Db 886 HisLeuGluHisGlyHisGlnProCysArgGlyGlySerGlyGlnGlyArgArgAlaAla 905

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QY 1713 GCTGGATATGCCGTGGCCACAGAGCTGGCCGAGTGCCT-----GGCCAGCAGGT 1763
Db 906 GlyAlaValArgArgGlyProPheAlaProArgHisAlaAspArgLeuGlyAlaGly 925
QY 1764 TGCCCCGGCGGCATCGT-----CATCGCGCTCCGCTCCCT 1802
Db 926 LeuGlyGlyGluHisArgProAlaAlaLeuArgProGlyGlyAlaHisCysArgGly 945
QY 1782 -----CATCGCGCTCCGCTCCCT 1802
Db 946 ThrValLeuAspProAlaValAspLeuArgHisGlyPheHisAspAlaLeuCysAlaAsp 965
QY 1803 CAGCCCGCCCTACCGCAGCTGATCCAGAA----- 1832
Db 966 ValProGlyLeuArgProProAlaProArgProAlaSerThrAlaLeuProAspAla 985
QY 1833 -----GGCGGGCTTCAGCTGCCTG----- 1853
Db 986 AlaGlyArgProProGlyGlnSerLeuGlyAlaValArgAlaAlaCysAlaGlyArg 1005
QY 1854 -----CATCCGCGCGCCACTCAGGGCTACATGACCGCGTCAACAT 1895
Db 1006 HisLeuProValArgArgHisProArgAlaAspGlyLeuGlyLeuArgArgGlnAsp 1025
QY 1896 GTACAGCTCCTTCTACATGGCCCGCGGAGGGGCGC 1931
Db 1026 ArgArgArgGlyAlaGlyProGlyArgGlyArg 1037

RESULT 11
US-09-252-991A-23774
; Sequence 23774, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23774
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23774

Alignment Scores:
Pred. No.: 1,66e-14 Length: 798
Score: 309.00 Matches: 213
Percent Similarity: 30.4% Conservative: 33
Best Local Similarity: 26.3% Mismatches: 255
Query Match: 8.5% Indels: 309
DB: 2 Gaps: 47

US-10-620-914-44 (1-1947) x US-09-252-991A-23774 (1-798)
QY 1933 TGGCGCCCTTCCGCGGG-----CCATGTAGAAGGAGC 1901
Db 16 TrpProMetAlaGlyGlySerMetAlaCysValAlaArgTrpThrProCysArg----- 33
QY 1900 TGTACATGTCAGCGGTCCATGTAGCCCTGAGTGGCGCGCGGATGACGGCGCAGTCA 1841
Db 34 -----ArgGlySerCys-----ArgTrpLeuAlaHisCysArgLeuArgSer 47
QY 1840 AGCCCGCCCTTGTGATGAGTCCGGTAGGGGGGCTG-----AGG 1800
Db 48 ValProArgSerGlyArgAlaSerArgSerThrTrpCysThrAlaProProVal 67
QY 1799 GAGCGGAGCGCCAGATGACGATGCCCGCGCGCAACC-----TGCTTGCC 1752
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Db 68 SerThrThrArgLeuAlaThrValProProThrSerThrAlaCysAlaMetCys-TripAl 87
QY 1751 AGGCACATCGGCCAGCT----- 1736
Db 87 aGlyCysArgProAlaAlaSerGlyProGlyAlaCysCysSerSerProAlaProGlySe 107
QY 1735 -----CGTTGGCCACGGGCATA 1719
Db 107 rThrArgArgProMetAlaAlaGlySerThrArgSerArgArgPheProArgSerIl 127
QY 1718 TCCA-----GCCAGTCCACGTGTCATCAGATCACCTTGGTGT----- 1679
Db 127 eProAspGlySerCysSerThrProSerArgSerArgTrpThrAlaGlyTyArgLeuPr 147
QY 1678 -AGTGGCGCGCTTTCAGCTCCTCATGAGAGAGTGGTGGAGACGGTTCAGTTGCCACC 1620
Db 147 oAlaCysAlaTrpProAlaSerThrValArgGly-----GlySerGlyCysSerTh 164
QY 1619 ACGC-----CACTCTTGAGGGTGG-----CGAAGGCGC----- 1592
Db 164 rArgCysValArgGlyThrGlyTrpSerAlaSerArgProCysMetProThrGlySerTh 184
QY 1591 -----CCTCGCGCAGGTAGTGGCGCAGTTGTGCGCAGGAACCTTCCCGTGAAGCAG 1539
Db 184 rProThrMetArgProGlyCysTrpProSerCys-----CysAlaProMetPr 200
QY 1538 TTGTAGTAGAAGTAGTCTGCTTGGCGCAGTCTCGCCAGTCTCGCCACCGCTCCATGG-- 1481
Db 200 oAlaAlaArgArgTrpArgThrAlaThrSerValSerThr-----ThrArgProTrpAr 218
QY 1480 -TGCGCGCGA-----TGATGTTCTCAATGG--GGATGCGCTCGCGCTTGATC 1437
Db 218 gCysThrArgTrpSerThrThrCysAlaSerAlaTrpAlaSerAlaGlyProThrAs 238
QY 1436 AGCCGCTACTGCTTCCCGCAGCCCGCGCCGACCAACACAGACGGCTTGTGAAGAGC 1377
Db 238 nileArgTyAlaAlaProAlaAlaSerValAlaAlaThrAlaAlaProGly--ArgSe 257
QY 1376 ACCAGGCTCAGAACTTGACAGCAGCAGCAGCGCTGGGCCCTTCTTCACGAG 1317
Db 257 rAlaGlyCysArg-----AlaileProAlaThr--AlaArgAlaThrArg-- 271
QY 1316 TGGATGAGCATGTTGCTGCCACAGACGGCGCTCTCTCCATTG-----TGGGC 1266
Db 272 -----ArgCysSerGlyThrProAspGlyCysGlnProValValGlyAlaSerLeuAl 289
QY 1265 GCGTTGGCGAGCGCTTGACGGTCTTGGCCAGTCCCGACACACAGCCAGGACCTGCAGC 1206
Db 289 aAlaTrpArgGlyAla-----ValProCysGlyLeuLeuArgProGlyValArgPr 306
QY 1205 ACCCAGC----- 1199
Db 306 oProGlnProPheGlyLeuArgHisArgLeuAspProProArgArgArgArgLeuProva 326
QY 1198 -----ACAGCTTGGCCATGCCCGCTTGGT-----AGTACAGGCGCGTCC 1161
Db 326 lProArgAlaAlaProCysAlaAlaGlyArgHisProValAlaAlaAspGluProGlyArgAl 346
QY 1160 TGAAGTACAGAGCGCTTGGACAGAGTGTGGCTGG-----TTTGGCAGCAGG 1110
Db 346 a---ThrTyArgAlaArgArgilleArgAlaAlaGlyLeuProAspAlaLeuCysArgGl 365
QY 1109 AAGGGCGCCAGCTTCTTCGTACAGCTCCTCAATGGCGGGTGCACGCCCTCGCCGAGC 1050
Db 365 yAsnAlaProAlaAlaArgPro----AlaArgProGlnThrValAlaAlaArgLeuArgTh 384
QY 1049 AGCTGCCACAGCTCCTCAAACTCCAGCTGTGTAATGGCCACCTTCTTCAGCTCCAGAAGC 990
Db 384 rGluProGlyArg--ArgArgGlnArgGlyGlyTrpProGlyValAlaGlyArgGlyPh 403
QY 999 GCGCAGTGGCGGGTTCAGTCCAGCCAGCACCT----- 953
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Db 403 eProAlaGlnArgArgIleGlyValGlyLysProProAlaGlyLeuAlaArgThrGlyLe 423
QY 952 -----GCCCGCCCTTCACACAGCAGGTTCCAGGCATTCCAGCGCGCTAGTCAGG 900
Db 423 uArgAlaSerArgArgLeuAlaProGlyGlyArgGlyAlaProArgArgArg----- 440
QY 899 GTCAGCACGCTGCTCTGGGGTTGATCTCCATCACCCTCCATATCCGGCTCGGGGTCCTCC 840
Db 441 -----AsnHisArgThrProAlaArgLeuProG1 450
QY 839 CACGACTCGTGTACAGGAAGTGGCG-----GGAACATGGCGCGCTCCACG 789
Db 450 ySerAlaCysTyrArgGlyAlaArgSerGlyProThrGlyAlaValAlaAlaProPr 470
QY 788 CGCTCTCTGTCAGGCGCTGGCCAACTGGCGCGGCCCAATCCACACGCTAGTAGGGG 729
Db 470 oAlaPro-----ProAspArgG1 476
QY 728 GCGCGCACCGCACGTAGGGGATCGAACCTGGGTGTTCTGTCTCCACACGCGCTCC 669
Db 476 yPheProAlaCysLeuArgArgAlaAlaAlaTyrLeuProThrAlaMetProGlyAlaPr 496
QY 668 AGCTTCTGCTCA-----GGTAGCGCGCGCTCGGGCGCGATGTCATGTTGTCGATG 615
Db 496 oGlyGlnAlaProValAlaGlyArgThrAlaAlaGlyGlyThrArgProAlaProArgLe 516
QY 614 TCGAAGATCGATCGCCAGA----- 596
Db 516 uLeuArgProGlyAlaLeuLeuHisAspLeuProAlaPheHisArgGlyHisSerGlyAl 536
QY 595 -----AGAAACGGCGCACCGAGGATCTGG 570
Db 536 aValProAlaGlnArgGlnAspLeuSerPhePheGlnTyrGlyAlaArgArgAlaAlaG1 556
QY 569 CGCAGGCGCAGTGTACTTGCCTCA-----CGTAGAAGTCGGCA 528
Db 556 nThrGlyLeuArgValSerArgGlyLeuHisValArgArgValArgProCysArgG1 576
QY 527 ACGGCCA-----CCAGGCGCTTGGACAGGTACGACAGCCTGGTCGATGACG 477
Db 576 nTyrProPheArgArgProAlaValAlaGlyAlaGlyLeu----- 589
QY 476 TTGTGAAACGTGGAATCATCGTAGCGAGTAGGAGAAGGTGATGAGCGTCGCGGTGCC 417
Db 589 ----- 589
QY 416 TCAGGGGCGCAATTCGACAGCGTCGCGCTCCACGACCTCGACATTTCTCCAGCCCTTG 357
Db 590 -----LeuProValGlyAlaArgArgPro----- 597
QY 356 GCCTTCGCTTCTTCTGGCCACCTCGCACAGCGAGTGGCACAGCTCGACACGCTAGATG 297
Db 598 -----AlaAlaArgPro----- 601
QY 296 GACTTGAACTTCGACAGTCGATGTAATCAGCCATCATATCGACATTTCTCCAGTGCCA 237
Db 602 -----AlaProGly-----ArgArgGlyGlyArgArgHi 611
QY 236 CCACCCAGGTCAA-----CCACATGAGTTTCAGCGCTCGGCGAGCGGGCAGCAA----- 185
Db 611 sArgProGlyGlnProProGluHisAlaAlaGlyAlaArgProValGlyGlnArgAlaG1 631
QY 184 -----AGGACAGCGG-----CCTGGGCGCGTAGAAGC----- 158
Db 631 yLeuGlyAlaGlnArgLeuAlaLeuAlaAlaGlyAlaArgArgThrValLeuProLeuAl 651
QY 157 -----TCTCCAGCGCAGCAGCGTATCATPCGCTTCTTTCGCGCAACACCATATGGCGC 102
Db 651 aglyGlyProGly-----AlaAlaCysAlaGluAlaThrGlyAsnAl 665
QY 101 AGACGGTCAGGTATCTCTTCATGCTGCTGAGCTTGAGCTTCTCCAGGAGAAAGTTCTTC 42
Db 665 aglyAlaAlaArgArgPro-----ValProArgArgLeuSerAl 678

QY 41 TTGGTGTAGCTCGCAGCGCGCC 19
Db 678 a-ArgAlaAlaArgArgProAla 685
RESULT 12
US-09-252-991A-17508
; Sequence 17508, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17508
; LENGTH: 1064
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17508

Alignment Scores: 2,21e-14 Length: 1064
Pred. No.: 308.00 Matches: 215
Score: 33.9% Conservative: 43
Best Local Similarity: 28.2% Mismatches: 267
Query Match: 8.5% Indels: 237
DB: 2 Gaps: 44

US-10-620-914-44 (1-1947) x US-09-252-991A-17508 (1-1064)

QY 149 GCCTGGAGAGCTTCTACGGCCCGCAGCGCTGCTTGTCTGCTGCC----- 193
Db 9 AlaTrpSerAlaAlaAlaTrpProTrpProAlaSerSerSerProCysSerSerCys 28
QY 194 ---GCCTGGCGCAGC-----GCTGAACCTCATCTGGGTGACCTGGGTG 235
Db 29 CysAlaTrpProSerAlaProProGlyProAlaThrAlaCysSerCysCysSer 48
QY 236 GTGCACCTGGGAGATGTCGATATGATGCTGATTACATCGACCTGCGAAGTTCAAGT 295
Db 49 AlaAlaCysSer-----CysSerAlaTrp---AlaCysSer 59
QY 296 CCATCTACGTGTGCTGACCTGTGCCACTCGGTGTGCGAGGTGGCCAAAGAAGCGAAGG 355
Db 60 AlaSerThrSerGlyAlaCysThrAlaThrCysAlaArg----- 72
QY 356 CCAAGGCTGGAAGAATGTCCAGGTGCG-----TGGAGGCGCAGCGCTTGCCAAATTGGCGC 409
Db 73 -----GlyArgAlaSerSerSerAlaTrp-----SerAlaGlnArg 85
QY 410 CCCCTGAGGCGCAGCGCTCATCA-----CCTTCTCTACTCTGCTCAGCATGATTC 463
Db 86 ProProArgPheProArgProCysSerGlyProValSerProLeuHisProAlaSerLeu 105
QY 464 CACCGTTCCCAACAGCTCATCCACGAGCTTCTGCTACTCTGCTCCCAAGA----- 512
Db 106 ProArgHisAspLeuGluSerArgArgLeuArg-LeuProArgHisArgLeuHisArgTy 125
QY 513 -CGCCCTGGTGGCGGTGCGGACTTCTACGTGAGCGGCAAGTACGACCTGCCCTGCCGCC 571
Db 125 rArgSerProAlaGlnCysArgLeuArgAspArgArgLeuHisProCysArgArgPr 145
QY 572 AGATGCCCTGTCGCGCGTTCCTTCTTCTGCGCATCGATCGATCGACACATTCGACA 631
Db 145 oThrGlyLysHisLeuLeuArgLeuGlyArgThrProLeuCysArgAlaArgHis----- 163

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QY 632 TCGGCCCGAGCGCGCTACCTGGAGCAGAGCTGGAGCGCGTGTGGAGCAGAACCA 691
Db 164 -----SerAlaalaArgAlaArgGlyArgGluProSerAlaValAlaGlyAla--Hi 180
QY 692 CCCAGGGTTCGATCCCTACGTGCGTGGCTCGCGGCCCTACTACGTGTGGATTGGCC 751
Db 180 sProProThrAlaPro-----GlyLeuProValLeuLeuLeuLeuProPr 195
QY 752 GCCTGCCAGGTGGCCACGCGCTTCACGA-----GGAGC 787
Db 195 oProAlaArg-----ArgAlaAlaArgLeuArgThrArgArgLeuGlnProAl 213
QY 788 CGCTGGAGCGCGCCCATGTTCCGCCCATCTCTGTACACGCGAGTGTGGAGGACC 847
Db 213 aArgPheAlaAlaAlaLeuProArgThrSerProGlyGluLeuGlyAlaGlyGlnAr 233
QY 848 CCGAGCCGGATATGAGGTGAT-----GGAGATCAACCCCAAGGACCGTGTCTGA 898
Db 233 gArgAsnAlaAspArgGlyAspProAlaSerHisAspArgAlaArgArgHisArgAlaAs 253
QY 899 CCCTGACTAGCGCGGTGCAATGCTGCACTGCTGCTGTCGCGGGGCCCGCCAGGTGG 958
Db 253 p-----ProArgProAlaGlyArgArgHisArgProArgGl 265
QY 959 TGTGGTGGACTGCAACCCCGCGCAGTCGCGCTTCTCGA-----GCTGAAGAAGGTGG 1012
Db 265 yThrArgPro---GluProAlaArgGlnAlaGlnGlyArgGlyCysProAlaAlaAr 284
QY 1013 CCATTACGACGTGGAGTTTGAGGACGTGTGGACGTGTCGCGAGCGGT-----1064
Db 284 gGlnProAlaAlaAlaArgProArgArgAlaAlaGlySerArgAlaGlyArgGluProGl 304
QY 1065 -----CCACCGCGCATTTAGGAGCTGTAGGAGAGCTGTAGGAGAGAGCTGCGCCCTCTCTGT 1114
Db 304 yGlnProLeuArgProAlaHisProGly-----313
QY 1115 CGCAACCGCAGCACAACTTCTGGTCCAAAGCGCTCTGGTACTT-----1157
Db 314 ---GlyArgProAlaArgLeuAlaGlnAlaGlyThrAlaValValArgProGlyAlaAr 332
QY 1158 -----CCACGACGGCT-----GTACTACGAGCGCGCATGGCGCAAGCT-----1196
Db 332 gGlyAspProAlaLeuProTArgLeuLeuProGlyArgArgThrGluAlaAspArgLe 352
QY 1196 -----1196
Db 352 uGluArgArgGlyArgArgGlnProArgSerArgAlaGlyGlnArgThrValLeuAr 372
QY 1197 -----GTGCTGGTCTGCA-----1211
Db 372 gProAlaAlaAspArgLeuArgArgGlyLeuAlaGlyAlaAlaLeuArgProAlaArArgAr 392
QY 1212 -----GTGCTGGCCCT-----GGTCTGGACTGGCGCAAGACCG 1246
Db 392 gAlaArgProValProGlyArgHisAlaThrGlyHisArgAlaGlyProGlyArgGlyAr 412
QY 1247 TCAGCGCCT-----CGCAACGCGCCACATGGAGGAGCGAGCGCCCTC 1291
Db 412 g---AlaProAlaTrpArgGlyValArgProAlaProHisAlaGlyAlaAspProAr 431
QY 1292 TGTGGGACGACCAATGCTCATCTTCATCTCGTGAAGACGCGCCCAAGCGCTGTGTGGC 1351
Db 431 gGlyGlnArgLeuHisArgGlnPro-----ProValArgThrProAlaAlaArgArgSe 449
QY 1352 TGTTTCGTCAGTTCTGTAGCCTGTGTCTTTCAA-----CAAGCGCGTGC 1396
Db 449 rLeuArgGlyProArgHisGlyHisArgLeuArgArgHisArgThrAlaGlnGlyArgPr 469
QY 1397 TGTG-----GTTGGCGCGCGCT-----GC 1417
Db 469 oAlaPheProLeuArgArgArgArgHisArgHisProPheGlyValAlaAlaArgGleProCy 489
QY 1418 CGGCAACGACGTAGCGCTGATCAAGCGGCGGATCCCATTTGAGAACTACATCGCGC 1477
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Db 489 sGluGluMetArgArgAspProAlaAlaGlyGlyHisArgHis-----AlaHisArgVa 507
QY 1478 GCAC-----CATGACCGCTGGCGGAGAACTCGCAGTGGCGAAGCAACT 1525
Db 507 lHisAlaGlnProAlaAlaGlyValArgThrGlyLeuArgGlyLysProAlaAspArgPr 527
QY 1526 ACTTCTACTCAACTGCCTCAC---CGCAAGTTTCTCT-----GGCGCAACTGCCCCA 1576
Db 527 oLeuLeuArgGluLeuArgGlnThrArgGlyValProPheHisLeuArgGlyLeuArgHi 547
QY 1577 CCTACCTGCGGAGCGCGCTTCGCCACCTCAAGAGTGGCTGTGGACAACTTGACCG 1636
Db 547 sValProGlyProGlyLeuArgArgProLeuGlu---ProGlyGlyArgAlaAspGl 566
QY 1637 TCTCCACCACTTCTTCATGGAGAGCTCAAGCGCG-----1673
Db 566 nGlnAlaAlaLeuAspLeuLeuGlyValGlnAlaValAlaArgProGlyAspLeuGlyLe 586
QY 1674 -----CACCTACAC-----CAAGGTGATTCTGA 1696
Db 586 uArgProAlaGlyProAlaLeuHisProValProSerValGlnLeuAspGlyProAlaPr 606
QY 1697 TGGACCACTGGA-----CTGCTGGA-----TATGC 1723
Db 606 oGlyProProGlyPheGlyAlaAspArgGlnLeuAlaGlyAspHisProAlaHisProAl 626
QY 1724 CCGTGGCCACGACGCTGCGCGAGTGTGGCCCAAGCAGGTGCGCC-----1769
Db 626 aProGlyArgArgHisAlaAspProProGlyArgArgArgAlaGluAlaLeuLeuHi 646
QY 1770 ---GGCGCGCATCTCATCTGCGCTCCGCTC-----CCTCAGCCGCGCT 1813
Db 546 sArgArgArgArgArgHisArgGlyProArgAlaAspHisArgGlnProArgArgProLe 666
QY 1814 ACGCCGAGCTGATCCAGAGCGCGGCTT-----CGACGTGCGTGCATCCGCGCGCCA 1867
Db 666 uArgArgAlaAspArgGlnHisArgGlnProGlyGlnArgGlyGlnHisProProAlaAr 686
QY 1868 CTCAGGCTACATGACCGCGCTCAACATGTACAGCTCTCTTACATGCGCGCGGAAGG 1927
Db 686 gArgGlyThrAlaAlaPro-----ValArgGlyProProAlaAl 699
QY 1928 GCGC 1931
Db 699 aArg 700

RESULT 13
US-09-252-991A-20408
; Sequence 20408, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20408
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20408

Alignment Scores: 2.31e-14 Length: 957
Pred. No.: 307.50 Matches: 224
Score: 34.6%
Percent Similarity: 32
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Best Local Similarity: 30.3% Mismatches: 280			
Query Match: 8.5% Indels: 204			
DB: 2 Gaps: 40			
US-10-620-914-44 (1-1947) x US-09-252-991A-20408 (1-957)			
QY	29	CGAGCTACACCAAGAGACTTCTCCCTGGAGAACTCAAGCTCAGCAGCATGAAGGATG	88
DB	128	ArgArgProAlaAArgArgThrArgPro-----	136
QY	89	ACCTGACGCTTCTCGCGCATATGTTGGTTCGGCAGCAAGAAAGGCGCATGATCAGCGTGTCTC	148
DB	137	-----LeuProGlyProAlaAlaSerProAla-----ThrGly	147
QY	149	GCCTGAGAGCTTACCGGCCCC-----AGCCGCTCCCTTTCCTGCTGCCGCC	196
DB	148	AlaGlyAArgLeuProProGlyProGlyArgGlyAlaAArgProLeuProAlaAlaProPro	167
QY	197	TGGCCGAGGCTCGA-----ACCTCATCTGGTGTGACC	229
DB	168	GlnSerProAlaAArgGlyProGlyAlaAlaGlyHisGlnProAlaAlaAlaGlyLeu---	186
QY	230	TGGGTGGTGGCACTGGGAGATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGT	289
DB	187	-----AlaProGlyAlaProAlaProValAlaAlaAlaAArgThrGlnArgThr	203
QY	290	TCAAGTCCATCTACGTGGTCGACCTGTGCCACTCGCTGTGCGAGGTGGCCCAAGAAAGG	349
DB	204	GlyProAlaProAspAArgGlyGluAArgGlyAlaAAspGlyAArgGlnAArgProArgThr	223
QY	350	CGAGGCCAAGGCTGGGAAGATGCCAGGTCTGGAGGCCGACGCTTGCCAAATTGGCG	409
DB	224	ArgArgGlyAArgAlaGlyAArgAlaAlaAArgAlaGlnAArgLeuGlyAArgAArgAlaAla	243
QY	410	CCCTTGAGGACCGCGGCTCATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	469
DB	244	ProLeuAlaAlaGlyAlaAArgAArgSerAArgGlyAlaGlyGlnProArg-----	259
QY	470	TCCCAACGTATCATGACAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	524
DB	260	-----GlyThrAArgAArgAArgThr-AspProArgLeuProAlaGlyGlyGly	275
QY	525	-----CGTTGCCACTTCTACGTGACGCGCAAGTAGCAGCTGCCCTCTGCCAGAT---	577
DB	275	YAspAArgAlaAlaAlaAArgGlyProGlyVal-----ProArgProAspArgAl	292
QY	578	CCTGTCTCGCGCTTCT	637
DB	292	AlaArgAla-----LeuLeuAArgAArgAlaAArgGlyAArgAArgGlyAArgGly	310
QY	638	CCGA-----CGCCGCGCTTCT	673
DB	310	nArgGlyAspProArgProProAlaAlaAArgProGlyLeuProAArgAlaAlaGlyAArgLy	330
QY	674	CGGT-----GTGGAGCAGAACACCC	694
DB	330	sArgProValValProLeuProProValLeuAArgProAlaAlaGlyAlaSerLeuAl	350
QY	695	AGGTTTCATCCCTACCTGCGCTGCGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	754
DB	350	aArgLeuAArgSerValAArgAArgLeuProAlaProAlaAArgLeuAArgLeuValGlnProPr	370
QY	755	TGCCAGCGTTGGCCACGCTCTGACGAGGAGCGGTGGAGCGCGGCCGCCAT-----	806
DB	370	O-----TrpProAlaAArgProGlyGlyAlaGlyAlaAArgAArgProAlaGly	387
QY	807	-----GTTCCCGCCACCTTCCTGTA-----CACCGAGTCTGGGAGGA-----	845
DB	387	YArgGlyGlyGluProGlyAlaGluProValGlyAArgAlaThrAlaGlyGlyAlaGluHi	407
QY	846	-----CCCCGAGCGGATATGGAGGTGATGGAGATCAACCCCAAGGACACGCTGTCTGA	898
DB	407	sArgHisProAlaAlaLeuGluAAspGlyProAlaGlyGlnProProGlyGlyGluHisAlaAl	427
QY	899	CCCTGACTAGCGCGGCTGCAATGCTCCCTGAACCTGCT-----GFTGCAAGG---GG	946
DB	427	aProAsp-----ProAlaValAArgLeuGlyAlaGlyAlaGly	439
QY	947	CGCGCCAGGTGTGTGGTGGACTGCAACCCCGCGCAGTCGCGCTTCTGGAGCTGAAGA	1006
DB	439	YLeuProAlaGlyCysAArgGlyAArgThrGlyAArgProThrGlyAlaAlaPheProAlaGlyAl	459
QY	1007	AGGTGGCCATTGAGAGCTGGAGTTTGGAGGAGCTGTGGCAGCT-----	1049
DB	459	aGlyAArgValAArgAlaAlaAArgProAlaGlyProValAlaGlyProGluAArgGlyAAspAr	479
QY	1050	-----GTTCCGCGAGGCGTGCACCCCGCGCATGAGGAGCTGTGACGAGA	1093
DB	479	gAlaAArgProAArgAArgTyAArgGlnGlyAArgGlyAlaLeuProAArgGlyLeuAlaGlyPr	499
QY	1094	AGAGCTGGCGCCCTT-----CCTGTC---GCAACACCGCCA-----	1127
DB	499	oAArgAArgGlyAlaLeuTrpHisProProAlaMetProValAAspAlaGluGlnProGlyGly	519
QY	1128	-----CAACTTCTGGTCCAAAGCGCTCTGTACTTCCAGCAGCGCCT---GTACT	1174
DB	519	YAspProTrpAArgLeuLeuAlaGlyAlaGlnLeu---GlnProAArgAArgProGlyValAr	538
QY	1175	ACCAGGCGGCATGGCAAGCTGTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1234
DB	538	gProAlaLeuAArgGlnProAlaVal-----AArgGlyThrGlyPr	551
QY	1235	TGGCGCAGACCGTCAAGCGCCT-----CGCCACCGCGCCACATGGAGGAGC	1282
DB	551	oLeuAArgProAArgProAArgProProGlyAlaAArgAArgGlyGlyAlaAArgAArgGlyGly	571
QY	1283	AGCGCGCTCTGGGA-----CAGCAACATCTCATCCACTCTCTGTAAGAAGC	1330
DB	571	YAlaProGlyProGlyThrProProAlaProAlaGlyAlaThrProLeuAArg-----Gl	589
QY	1331	GGCCCAAGCCCTGGTGTGCTGTTGTTCAAGTTCGTGAGCTGTGTCTTCTTCAACAAGG	1390
DB	589	YAlaAArgAlaAlaProAlaValProAArgLeuProAlaGlnProGlyAla-----	605
QY	1391	CCGTGCTGTGTTGGCGCGCGCTGCGCGCAAGCAGTACGCGCTGATCAAGCGGAGC	1450
DB	606	-----AlaAlaGlyAArgSerAlaGlnValAAspGlnAlaGlyAs	618
QY	1451	GCATCCCTTATGAGAACTTACATCGCGCGCACCATGGA-----CGCGCTGGCGGAGA	1501
DB	618	nArgGlyAsnProGlnLeuProGlyCysGlnProGlyAAspAArgLeuAArgProGlyGly	638
QY	1502	ACTCGCAGCTCGCAAGCAGAACTTCTTCTACTCAACTGCT-----CACCGCA	1552
DB	638	nProGlyAArgAlaProGlyGlnLeuAArgGlyGlyValAArgProAlaTrpAArgAArgAl	658
QY	1553	AGTT-----CCTGCGCAACTGCCCCACCTACCTACCTGCGCGAGGCGG	1594
DB	658	aValAAspAlaCysLeuGlyTyProAlaAAspLeuLeuPro-----Gl	672
QY	1595	CCTTCGCCACCTCAAGAGTGGCT-----GGTGGCAACCTGACCGCTCTCCACCA	1645
DB	672	YGlyAAspHisProAspGlnValAArgThrLeuAlaGlyProGlyProAAspAArgThrGlyAr	692
QY	1646	ACTTCTTCATGGAGAGCTCAAGCGCGCACTTACACCAAGGTGATTCTGTATGGACCAAG	1705
DB	692	gArgLeu-----AlaThrAlaProGlyAArgHisLeu-----Ar	703
QY	1706	TGGAGTGGCTGGATATCCCGTGGCCCAACAGTGGCGAGTGGCTGGCCCAAGCAGGTG	1765
DB	703	gTrpAlaGlyGlyHisAlaAlaGlyMetGlnSer-AlaAlaAlaAlaCysGlyValA	723
QY	1766	CGCGCGCGCATCGTCTATCTGGCGCTCG-----CCTCCCTCAGCGCGCCTACG	1816
DB	723	laProGly-Arg-----ProGlyAlaProAArgThrProGlyGlySerAArgProAla	740

QY 1817 CCGAGCTGATCCAGAGCGGGCTTCGACGTGCGCTCATCCGCGCGCCACTCAGGCT 1876
|||
Db 741 Pro-----GlyProAlaGlyProLeuAspAla 749
|||
QY 1877 ACATGGACCGGTCAACATGTACAGCTCTTCTCATGCGCCCGCGGAGCGC 1930
::|||
Db 750 GlyGluArgArgValAlaAlaGlySerProGlyProArgProThrGlyArgAla 767
|||
RESULT 14
US-09-252-991A-18035
; Sequence 18035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: 1999-02-18
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18035
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18035

Alignment Scores:
Pred. No.: 4,58e-14 Length: 783
Score: 303.00 Matches: 225
Percent Similarity: 35.2% Conservative: 45
Best Local Similarity: 29.4% Mismatches: 277
Query Match: 8.4% Indels: 220
DB: 2 Gaps: 45
US-10-620-914-44 (1-1947) x US-09-252-991A-18035 (1-783)
QY 1945 AGTTGTCTCTTGGCGCCCTTCGCGGGCCATGTAGAAGAGCTGTACATGTTGACGC 1886
|||
Db 2 SerLeuProThrAlaArgPro-----ArgSerArgGlyAlaAspArg 15
|||
QY 1885 GGTTCATGTAGCCCTGAGTGGCGGGCGGATGACGCGCAGCTCCAGCGCCCTTCTGGA 1826
|||
Db 16 GlnProThrGluPro-----AlaArg-----ProProAlaAla 26
|||
QY 1825 TCAGCTCGGCGTAGGGCGGCTGAGGAGG---CGGAGCGCAGATGACGA----- 1778
|||
Db 27 GlyArgArgValProAlaGlyLeuGlyArgGlyArgAlaValGlnProArgProAlaGly 46
|||
QY 1777 TGCGCCCG---GCGCAACCT-----GCGCAACCT-----GCTTGG 1754
|||
Db 47 LeuArgProCysLeuLeuHisProGlnGlyGlnArgAlaAspProLeuArgAlaVal 66
|||
QY 1753 CCAGGCACCTCGGCGAGCTCTGTCGCA---CGGCGATATCAGCGCAGTCCACGCTGCTCA 1697
|||
Db 67 ProAlaGluArgProAlaArgThrProGlyLeuAlaArgAlaGlyGlyGlyAla 86
|||
QY 1696 TCAGAAATCACCTTGGTGTAGTGGCGGCTTTGAGCTCTCCATGAAGAAGTTGTGGAGA 1637
|||
Db 87 ArgGluAspLeuAlaValArgGlyThrArgArgLeuProValAspArgArg---TyrArg 105
|||
QY 1636 CGGTACAGTTGTCACACAGCCACTCTTTAGGGGTG----- 1601
|||
Db 106 ArgAlaGlyArgArgArgProAlaProGlyLeuArgGlyIleGluGlyLysThrArg 125
|||
QY 1600 ---CGAAGCGCGCTCGCGCAGGTAGTGGGCGAGTGTCTCGCGCAGGAACCTTGGCGGTGA 1544
|||
Db 126 ArgArgArgProValArg----- 131
|||
QY 1543 GGCAGTTGTAGTAAGTAGTTCTGCTTGCAGCAGTGGAGTTCTCCGCCACGCGCTCCA 1484
|||

Db 132 -----GlnArgThrGlnAlaSerAlaAlaArgProSerAlaProHisArg----- 146
|||
QY 1483 TGGTGGCGCGATAGTTCTCAATGGGATCCGTCGCGCTTATCAGCGCGTACTGCT 1424
|||
Db 147 -----TyrArgGlnPheAlaGlnArgGlyGlyAspProArgHisGlnArgValSer 164
|||
QY 1423 TGCCCGCAGCGCGCCCGCAACACACAGCAGCGGCT---TGTTGAAGAGCACACGAGCTCA 1367
|||
Db 165 ProProSerThrAlaGlyArg-----AlaAspProGlyAlaHisArgSerProGlyPro 182
|||
QY 1366 CGAACTTTGACGACACGACACACAGCGCTTGGCCGCTTCTTCCAGAAAGTGGATGACGA 1307
|||
Db 183 ArgGlyArgArgThrAspArgProAlaAla---AlaThrGlyArgProAlaGly----- 199
|||
QY 1306 TGTGTCTGCCACAGAGCGCGCTCTCTCCATGTGGCGCGCTTGGCGAGGCGCTTG- 1248
|||
Db 200 -----LeuArgArgAlaAspProGlyProTrpArgArgPheProGlyArgPro 215
|||
QY 1247 ACGGTCTTGGCCAGTCCACGACACACGCGCC-----AGCAGCTGCAGCAC 1203
|||
Db 216 LeuValLeuGlnArgArgSerGlyAlaArgArgGlyGlyLeuArgHisAlaAspArg 235
|||
QY 1202 CAGCACAGCTTGGCCATGCCCGCTGTGTAGTACAGCGCGCTGTGGAAGTACAGAGGCGC 1143
|||
Db 236 GlnArgGlyArgProArg-----AspArgArg 244
|||
QY 1142 TTGACACCAAGTTGTGCTGTTTGGACAGGAGGCGCGCTTCTTCTCGTACAGC 1083
|||
Db 245 IleAspGlnArgLeu-----ArgArgArg-ArgAlaArgAlaAspAlaPheGlyArg 261
|||
QY 1082 TCCTCAATGCGCGGTGCACGCCCTCGCGCA---ACAGCTGCCACACGCTCTCAAACTCC 1026
|||
Db 261 gArgArgThrAlaGlyAlaGlnArgArgArgProAlaAlaSerArgArgProAlaPr 281
|||
QY 1025 AGCTGCTGAATGCGCCTTCTTCCAGTCCAGAGCGCGCTGCG----- 980
|||
Db 281 oAla-----ProGlyAlaAlaHisAlaArgProValAlaAlaArgThrProAl 297
|||
QY 979 -----CGGGTTGCACTCCACCGACACCACTTGGCGCGCGCTTCCACGAGGTTTC 927
|||
Db 297 aProGlyArgArgArgProProAlaProSerArgArgThrProAlaProAlaGlyAl 317
|||
QY 926 A-----GGGATTGCGCGCGCTAGTCAGGGTCAGCAGCGCTGT----- 887
|||
Db 317 aAlaProGlyArgProGlyHis-----AlaProAlaProCysLeuArg 331
|||
QY 886 -----CCTTGGGTTGATCTCCATCACCTCTCATATCCGGCTCGGGTCTCCACGACTGC 831
|||
Db 331 gAlaProAlaGlyGlyProProArgThrPro-----GlyProProGlyAspAl 347
|||
QY 830 G-----TGTCAGGAAGTGGCGGGAACATGGCGCGCTCCACGCGCTCC 783
|||
Db 347 aSerArgArgThrAlaSerGlyProHisProGlyAlaAlaProAlaGluAlaArgGlnPr 367
|||
QY 782 TCGT-----GCAGGGCTGCGCAACCGTGGCGAGCGCGCAATCCACGCTAGTAG 732
|||
Db 367 oArgArgAlaProAlaAlaArgArgProArgGlyThrGluGlySerSerSerAlaProAr 387
|||
QY 731 GGGCGCGCAGCCACGCGCATAGGGGATCGAACCTGGGTGTCTGCTCCACACGCGC 672
|||
Db 387 gArgThrGlyAlaAspAlaGlnArgGlyGlnProAlaGlyAspProGlyProArg----- 405
|||
QY 671 TCCAGCTTCTGCTCAGGTAGCGCGCTCGGGCGGATGTCAATGTTGCGATGTGCG 612
|||
Db 406 -----LeuGlnHisProProArgArgAlaTrpProGlyAsp-----ProArgCysAr 421
|||
QY 611 AAGATCATCGCC-----AGAAGAAACGCGCC 585
|||
Db 421 gProAspProAlaGlyThrAlaProGluGlyAlaProArgGlyArgArgThrGlyGlyAl 441
|||
QY 584 GACCAGGGCATCTGGCGGAGGGGAGGTCTGCTTGGCGCTCAGCTAGTAAGTCCGCAACG 525
|||

Db 441 aGlyArgGlyGlnProProAspAlaGlyAspProValAlaAlaGlyLeuSerArgAspAs 461
QY 524 CCACCAGCGCGTCTGGACAGAGTACGAGCAAGCCTGCTCGATGACCTGTGTGGAACGGT 465
Db 461 pProGlnProThrGly- 476
QY 464 GGAATCATCTGTCAGCGAGTGGAGAGGTGATGACGCTGCGGTGCTCCCTCAGGGGGCCCA 405
Db 476 oProArgPheSerAlaProArg- 491
QY 404 AATTGGCAAGCGCTGGCCTCCACGA- 491
Db 491 oLeuGlyHisGlnProAlaAlaArgGlnProGlyGlyThrSerArgArgAlaPro- 510
QY 347 TTCCTCTTGGCCACT- 317
Db 510 oAlaThrHisProAlaGlyArgGlyAlaTyArgGlyArgArgThrAlaGlyGlyAlaLe 530
QY 316 - 316
Db 530 uProProAlaThrGlyGlnArgArgGlyArgAlaValAlaSerValGlyProAlaGlyAl 550
QY 266 GCCATCATATCGACATTCCTCC- 236
Db 550 aAlaProGlyGlnGlyAlaProGlyGlyArgArgGlyLeuHisArgArgProAspLeuPr 570
QY 235 - 216
Db 570 oAlaIleAlaGluLeuHisProAlaLeuProAlaHisArgAlaGlyGlyProHisGlyAr 590
QY 215 AGTTTCGAGCGCTGGCGAGCGGGCAG- 170
Db 590 gGlyGlnArgArgArgGlyAlaGlyGlnGlyArgArgArgProGlyProGlyLeuAr 610
QY 169 - 138
Db 610 gProGlyArgGlyArgArgThrGlyArgAlaArgArgHisProAlaProArgProAs 630
QY 137 TCAT- 81
Db 630 pHisProArgGlnProCysProArgArgThr- 644
QY 80 ATGCTGTGACTTGAGCTTCTCAGGGAGAGTCTTCTTGTGTAGCTCGCAGGCGG 21
Db 645 - 661
QY 20 CCGTCACGACCCGACC 5
Db 661 sArgHisGlyProThr 666

RESULT 15

US-09-252-991A-26099
; Sequence 26099, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26099
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099

Alignment Scores:

Pred. No.: 5,65e-14 Length: 863
Score: 302.00 Matches: 227
Percent Similarity: 29.8% Conservative: 29
Best Local Similarity: 26.5% Mismatches: 252
Query Match: 8.3% Indels: 350
DB: 2 Gaps: 50
US-10-620-914-44 (1-1947) x US-09-252-991A-26099 (1-863)
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QY 1906 ---AGGAGCTTACATGTTGACGCGCTTCATGTAGCCCTGAGTGGCGCGCGATGACG 1850
Db 68 IleArgProCysLeuArgSerArgArgAspCysPhe- 85
QY 1849 GCAGCTCGAGCCCGCTTCTGGATCA- 1814
Db 86 SerHis- 103
QY 1813 AGG- 1805
Db 104 ArgGlyAlaValHisProArgLeuArgArgArgThrGlyArgArgAspProAlaAla 123
QY 1804 TGAGGAGG- 1769
Db 124 ArgGlyArgThrHisArgLeuProThrAspAspGlnGlnArgArgArgArgPro 143
QY 1768 GCGCAACTGCTGGCCAGGCACTCGGCCAGCTCGTTGGCCA- 1727
Db 144 ArgHisAlaProGlyGlyThrArgProThrAlaGlyProValAlaHisArgThrLeu 163
QY 1726 - 1715
Db 164 GlySerAlaGlyArgLeuArgGlnArgArgThrAspProGlyGluGlyArgAlaAlaPro 183
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Db 184 Ala- 195
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Db 196 - 210
QY 1594 CCGCTCGCGCAGGTAGTGGGCGAGTTGTGCGCGAGAACTTCCGCTGAGCGCAGTTGT 1535
Db 211 ProProGluGlyHisArgGlySerSerLeuProGly- 223
QY 1534 AGTAGAAGTAGTCTGCTTCCGCAACGTGCTTCCGCCACGCCCTTCCATGTTGCGCG 1475
Db 224 - 239
QY 1474 CGATGTAGTCTCAATGGGATCGCTCCGCTTGATCAGCGCGTACTGCTTGGCCGCGCA 1415
Db 240 ArgGlyPheGlyGlnLeuArgGlyArg- 248
QY 1414 CCGCGCGCGCAACACAGCAGCAGC- 1391
Db 249 ArgHisArgArgValSerSerArgArgGlyTrpProLeuLeuProGlyAspGluTyr 268
QY 1390 ---CCTTGTGTAAGACAGCAGGCTCACGAATCTTGACNAACAGCACACCGCGCTTGG 1334
Db 269 ProProAlaGlyArgThrProGlyHisArgThrGlyHisArgProGlyProGlyGlyLeu 288
QY 1333 GCCGCTTCTCACGAAGTGA- 1280
Db 289 AlaAspProArgArgGlyProSerAlaAlaAlaGlyThrGlyThrAla 308
QY 1279 - 1238
Db 309 ArgAlaCysHisArgGlyProProLeu- 323

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QY 985 ACTGCGGGGCTTCAGTCCACGACACCACTGCGCGGCCCTGTGCACACAGCAGGT--- 929
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QY 664 -----TCTGCTCCA-----GCTAGGCGC-----GGCGCTCGG 638
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QY 262 -----TCATATCCACATTCTCCCGAGTGCACCACCCAGGTCAACCCAGATGAGGT 212
Db 654 AlaHisValThrAlaArgGlnAspPro---ValHisHisArgArgGlnProArg----- 670
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QY 194 ----- 194
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QY 157 TCTCCAGCGCAG-----CAGCGTGATCATCGCCCTTCT 125
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Db 748 -----GlyGlnGlnArgArgGlyAspPro----- 755
QY 64 GCTTCTCCAGGAGAAAGTTCTTCTTGGTGTAGCTCGCAGCGCGCGCTCAGCAG 11
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Search completed: May 5, 2006, 07:53:02
Job time : 78 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 5, 2006, 07:51:18 ; Search time 28.5 Seconds
(without alignments)
5708.868 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

Sequence: 1 atggggcggtcggtgcagg.....gcgccaaagaagacaactaa 1947

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-MINMATCH=0.1 -LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA Main:

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3463	95.7	648	4	US-10-620-914-45
2	891	24.6	752	5	US-10-741-849-7021
3	850.5	23.5	908	4	US-10-620-914-50
C 4	476.5	13.2	19662	4	US-10-084-846A-6
5	459	12.7	19723	4	US-10-084-846A-5
C 6	457.5	12.6	19652	4	US-10-084-846A-7
C 7	456.5	12.6	19652	4	US-10-084-846A-7
8	446	12.3	19608	4	US-10-084-846A-8
9	443.5	12.3	19695	4	US-10-084-846A-3
C 10	436	12.0	19608	4	US-10-084-846A-8
C 11	424	11.7	19725	4	US-10-084-846A-4

12	407	11.2	19725	4	US-10-084-846A-4	Sequence 4, Appli
C 13	383.5	10.6	19695	4	US-10-084-846A-3	Sequence 3, Appli
14	379.5	10.5	416	4	US-10-118-495-3	Sequence 3, Appli
15	379.5	10.5	416	4	US-10-620-914-3	Sequence 3, Appli
C 16	370	10.2	900	5	US-10-450-763-33892	Sequence 336, App
17	366.5	10.1	1084	5	US-10-794-514A-336	Sequence 336, App
C 18	357	9.9	1084	5	US-10-794-514A-336	Sequence 336, App
C 19	352	9.7	599	5	US-10-450-763-33889	Sequence 33889, A
20	342.5	9.5	19662	4	US-10-084-846A-6	Sequence 6, Appli
21	341.5	9.4	437	4	US-10-437-963-132079	Sequence 132079,
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43	303.5	8.4	4440	4	US-10-176-482-525	Sequence 525, App
44	303.5	8.4	4440	4	US-10-176-757-525	Sequence 525, App
45	303.5	8.4	4440	4	US-10-176-913-525	Sequence 525, App

ALIGNMENTS

RESULT 1

US-10-620-914-45
; Sequence 45, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-45

Alignment Scores:
Pred. No.: 1.73e-204 Length: 648
Score: 3463.00 Matches: 648
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.7% Indels: 0
DB: 4 Gaps: 0

US-10-620-914-44 (1-1947) x US-10-620-914-45 (1-648)

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Db 1 MetGlySerGlyArgAspGlyArgProAlaSerTyrThrLysLysAsnPhenSerLeuGlu 20

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; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
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; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7021

; LENGTH: 752

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-741-849-7021

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 QY 604 TCGATCTTCGACATCGACCAATTCATCGGCCCGCGCGCGCTACCTCGGACGAG 663
 Db 250 IleTrpPheGluAlaAspLysValPheLeuAspSerSerArgAsnTyrLeuGluTyr 269
 QY 664 AAGCTGGAGCGCGTGGGAGCAGAACACCCAG-----GGTTCGATCCCCCTAC 711
 Db 270 LysPheGlyThrValLysSerLeuAsnSerTyrAsnLysAlaLeuGlyLysIle----- 287
 QY 712 GTGCCGTGGTGGCGGCCCTACTAGTGTGGATTCGCCGCTGCCAGCGTGGCCAC 771
 Db 288 -----ProTyrTyrIleTrpIleGlyCysAspLysSerLysSerHis 301
 QY 772 GCCCTGCACGAGAG-----CGCGTGGAGCGGCGGCCCATGTTCCCGCCACC 819
 Db 302 ThrIleLeuGluArgLeuAsnCysLeuAlaThrGluSerProTyrLeuAlaProThrThr 321
 QY 819 ----- 819
 Db 322 ThrProIleAlaAsnGlnLeuGluAspIleProIleSerLysGlyHisGluAlaAlaLeu 341

QY 819 ----- 819
 Db 342 IleAsnLeuGlnLysAsnLeuProTyrProSerMetTyrTyrGlnLysGluTyrTrpArg 361
 QY 820 -----TTCCCTGTACACG 831
 Db 362 ValTyrTyrAspGluMetAsnProLeuTyrGluGlnPheLysAsnGlnTyrIleTyrAla 381
 QY 832 CAGTCGTGGAGACCCCGAGCCGATATGGAGGTGATGGAGATCAACCCCAAGACACG 891
 Db 382 PheThrTrpGluAspProArgGluAspHisLysLeuLeuAsnPheThrSerAspAspThr 401
 QY 892 GTGCTGACCTGACTAGCGGGGCTCAATGCCCTCGAACCTG-----CTGGTCAGGGG 945
 Db 402 ValLeuAlaIleThrSerAlaGlyAspAsnIleLeuSerTyrAlaSerLeuProThrPro 421
 QY 946 GCCGGCAGGTGTGTCGGTGGACTGCAAGCCCGCAGTCGGCGCTTCGAGCTGAAG 1005
 Db 422 ProLysLysIleHisAlaValAspLeuAsnProCysGlnAsnHisLeuLeuGluLeuLys 441
 QY 1006 AAGGTGCCATTACAGCAGCTGGAGATTGTGAGACGCTGGCAGCTGTTCGGCGAGGGGTG 1065
 Db 442 LeuAlaSerPheArgCysLeuSerGlnGluGlnIleTrpSerMetPheGlyGluGlyLys 461
 QY 1066 CACCCGCGCATTTAGGAGCTGTACGAGAAGAAGCTGGCGGCTCTCTCTGTCGCAACACG 1125
 Db 462 IleGluAsnPheAsnAspLeuIleAspThrLeuAlaProHisMetSerSerAsnAla 481
 QY 1126 CACAACCTTCGTGGTCCAAAGCGC-----CTCTGGTACTTCCAGCAGCGCTGTACTACG 1179
 Db 482 PheGlnTyrTrpMetAspLysGlyProLysThrPheSerGlyLysGlyLeuTyr----- 499
 QY 1180 GCGCGCATGTCGAAGCTGTGCTGGTGTCTGCAGTGC-----CTGGCGGTGTGCTG 1230
 Db 500 ---AspThrGlyPheSerArgTrpAlaLeuArgLeuSerArgTyrValPheLysValCys 518
 QY 1231 GGACTGGGCAAGACCGTCAAGCGCTCGCCAAAGCGGCCCAATGGAGGAGCAGCGCGGT 1290
 Db 519 GlyValSerLysTyrValGluGluLeuCysAlaAlaThrThrMetGluGluGlnLeuArg 538
 QY 1291 CTGTGGGACAGCAACATCTCATCTTCTGTGAAGAAGCGGCCCAAGCGCTGTGTGG 1350
 Db 539 IleTrpAsnGluHisLeu-----LysProThr----- 547
 QY 1351 CTGTTCCTCAAGTTCTGTG---AGCCTGTCTCTTCAACAAGCGCTGTGTGTGCTGGC 1407
 Db 548 LeuPheAsnProValValGlySerLeuLeuValGlyAsnProMetPheLeuTrpLysAla 567
 QY 1408 GCGGGGTGGCGGCAAGAGTAGCGCTATCAAGCGGACGCGCATCCCATTTAGAAC 1467
 Db 568 LeuGlyValProAlaAsnGlnAlaLeuMet-----GlyProSerValIleLys 584
 QY 1468 TACATCGCGCGCACCATGGACGGGTGGCGAGAACTCGCACGTCGCAAGCAGCAACTAC 1527
 Db 585 TyrValValAspThrLeuAspProIleIleLysArgSerMetIleSerAsnAspAsnTyr 604
 QY 1528 TTCTACTACAACCTCACCGGCAAGTCTCTGCGGACAACTGCCCACTCTCTCTCTCT 1587
 Db 605 PheTyrTyrLeuCysMetMetGlyArgTyrThrLysAsnAsnCysProAspTyrLeuThr 624
 QY 1588 GAGCGGCTTTCGCCACCTCAAG-----AGTGGGTGGT 1623
 Db 625 ThrLysGlyPheAsnArgLeuSerSerThrAlaAlaThrAlaSerGlySerSerProIle 644
 QY 1624 GACAACCTGACCTCTCCCAACTTCTTCTCATCGAG-----GAGCTCAAGCGCGC 1674
 Db 645 AspAsnLeuArgIleHisThrAspThrLeuAsnGluValPheGlyArgLeuLysGluLys 664
 QY 1675 ACCTACCAAGGTGATTTCTGATGAGCAGCTGGAGCTGGCTGGAT-----ATGCCC 1725
 Db 665 SerIleThrIleAlaIleIleMetAspHisMetAspTrpPheAspProAsnGlyArgAsp 684
 QY 1726 GTGGCCAAAGAGCTGGCCGAGTGCCTGGCCCAAGAGGTTCGCGCGGCGGATCGTCATC 1785

Qy	1351	CTGTTCTGCTCAAGTTCGTGAGC---CTGGTGTCTTCAACAGGCGGTGCTGTGTTCTGGC	1407
Db	667	LeuLeuAsnArgPheValAsnGlyLeuValLeuSerSerAspAlaPheLeuTrpSerAla	686
Qy	1408	GGCGGCTTCGCGGCAAGTAGTACGCCTGATCAAGCGGAC-----	1449
Db	687	LeuGlyValProLysAsnGlnValAlaMetIleGluAlaAspTyrHisArgArgSerIle	706
Qy	1450	-----GGCATCCCATTTGAGAAC	1467
Db	707	SerSerSerThrThrProSerSerLysGluLysProSerArgAlaGluAlaIleLeuHis	726
Qy	1468	TACATCGCGGCACCATGGACGGCGGTGGCGAGAACTCGACGTGGCCAGCAGCATAC	1527
Db	727	TyrThrThrSerThrLeuAspProValLeuSerThrSerHisLeuAlaSerAspAsnPro	746
Qy	1528	TTTCTACTACAACTGCCTTCACGGCAAGTCTCTGCGCACTGCTGCCCACTCACTCTCGC	1587
Db	747	TyrTyrLeuValCysValLeuGlyGlnTyrThrArgGlnCysHisProAspTyrLeuSer	766
Qy	1588	GAGCGCGCTTCGCCACCCCTCAAGAGT---GGCGTGTGGACAACTGACCGTCTCCACC	1644
Db	767	ProAlaAlaHisSerIleLeuSerAlaProGlyAlaPheAspGlyLeuArgIleHisThr	786
Qy	1645	AACTTCTTCATGGAGGAGTCTC-----AAAGCGCGCACTACACCAAGGTGATTCTG	1695
Db	787	AspGluIleGlnGluValLeuAlaArgPheGlnProGlyThrLeuThrValAlaVal	806
Qy	1696	ATGGACCACCATGGACTGGCTGGATATGCC-----	1725
Db	807	MetAspSerMetAspTrpPheAspProProSerProGluGluGluLysGluGlyArgGly	826
Qy	1726	GTGCGCCAAAGAGCTGGCCGAGTGCCTGGCCAAAGCAGAGTTCGGCGGCGGATCGTCATC	1785
Db	827	LysAlaArgGluGlnValArgLeuAsnArgAlaLeuLysValGlyGlyLysValLeu	846
Qy	1786	TGCGGTTCGCGCTCCCTCAGCGCCGCTACGCGAGTGTATCCAGAGGCGGCTCGAC	1845
Db	847	LeuArgSerAlaGlyValGluProTrpTyrValArgValPheValGluGluGlyPheGly	866
Qy	1846	GTGCGCTGTCATC-----CGCGCGGCCACTCAGGCGCTACATGGACCCGCGTC	1890
Db	867	AlaArgArgValGlyCysArgGluSerGlyArgGlyAspGlnGluCysIleAspArgVal	886
Qy	1891	AACATGTACAGCTCTTCTACATGGCCCGCGG	1923
Db	887	AsnMetTyrAlaSerCysTrpIleLeuGluLys	897

RESULT 4

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US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE NUMBER: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:

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Db 12655 TrpGlyArgValAlaSerProAlaArgSerAlaAlaArgAlaProArgAlaProGlyAsn 12674
Qy 1210 GCAGCA-----CC 1202
Db 12675 AlaAlaProAlaThrAspProArgThrThrProArgProArgProArgArgPro 12694
Qy 1201 AGCAGCTTCCCATGCGCG-----CCTGTAGTACAGCGCTGCTGGA 1157
Db 12695 AlaArgCysProAlaAlaArgProAlaAlaArgProGlySerAlaGlyArgAlaGly 12714
Qy 1156 AGTACCAGAGCGCT----- 1142
Db 12715 SerProGlyValProProArgProProGlyArgAlaCysArgArgArgGlyAsp 12734
Qy 1141 -----TGG 1139
Db 12735 ArgAlaArgProArgProSerProProValAlaCysArgArgArgSerArgArg 12754
Qy 1138 ACCAGAGTTGGCTGGTT-----GCCAGAGGAAG 1106
Db 12755 AlaArgProCysGlyAlaAlaGlyGlyProArgArgProAlaAlaArgSerThrSerArg 12774
Qy 1105 GCGCCAGCTTCTCT---CGTACA-----GCTCCTCAATGCGCGGTGCA 1064
Db 12775 ArgProAlaAlaGlyProArgThrArgArgAlaAlaProGluArgAlaValHis 12794
Qy 1063 CGCCCTCGCCGACAGCTGCC-----ACACGTCTCTCAA 1031
Db 12795 ArgAspArgArgThrValAlaAlaArgSerAsnArgAsnArgSerArgValArgPro 12814
Qy 1030 ACTCAGCTGCTGAATGCCACCTTCTTCAGCTCAGNAGCGCGACTGCGCG---GGT 974
Db 12815 ArgProAlaAlaGlyArgProGlyArgGlyArgProValArgAlaGlyAlaArgProGly 12834
Qy 973 TGCAGTCCACCGACACCACTGCGCG-----CCCCCTGACACAGAGTTTCAGGGCAT 920
Db 12835 ProAlaAlaThrAlaProProAspArgArgGlyProAlaAlaArgProSerGlyProArgHis 12854
Qy 919 ---TGCAGCCCGCTAGTCAGGG---TCAGCACCGTCTCTTGGGGTGTATCTCCATCA 866
Db 12855 GlyArgAlaAlaArgGlySerGlyArgArgArgProArgProSerGlyArgProAlaAla 12874
Qy 865 CCTCATATCCGGCTCGGGTCTCTCCACGACTCGGTGTACAGAAAGTGGCGCGGAACA 806
Db 12875 ProProArgPro---ArgGlyArgPro-----GlySer 12884
Qy 805 TGGGCGCGCGCTCCACGCGCTCTCGTGCAGGGCGTGCCAAACGCTGGGACGGGCCAA 746
Db 12885 AlaAlaAspProProSerAlaPro-----GlyGlySer 12895
Qy 745 TCCACACGTAGTGGGGCGCGCAGCCACCGACAGTGGGATCGAACCTGGGTGTCT 686
Db 12896 SerSerCysProGlyGlyArgGlyAlaLeuArgProArgArgArgProProGly---Thr 12914
Qy 685 GCTCCACACCGCTCCAGCTTCTGCTCCAGGTAGG---CCGCGGCTCGGGC----- 635
Db 12915 ProProAlaAlaArgProGlyArgSerProArgArgGlyArgGlyCysProGlyThrGly 12934
Qy 634 -----CGATGTCATGTTGT-----CGATGT-----CGAAGA 608
Db 12935 GlyCysArgArgProAlaAlaCysCysAlaThrAlaAlaGlyArgCysProArgArgArg 12954
Qy 607 TCGATC-----GCCAGAGAAACGGCGCACGAG----- 578
Db 12955 AlaCysProAlaAlaCysGlySerArgArgGlyArgAlaAlaArgProLeuAlaProArg 12974
Qy 577 -----GCATCTGGCGCGCGGCGAGGTCTGACTTGC----- 548
Db 12975 ArgTrpAsnAlaThrAlaGlyGlyAlaAlaAlaArgGlyArgAlaAlaGlyLeuArgGlySer 12994
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Qy 547 -----CGCTCAGTAGAAGTCGGCAACGCCCCACCGCC 515
Db 12995 ArgSerAlaGlyAlaProThrSerProArgSerArgArgGlySerGlyArgArgProArg 13014
Qy 514 CGTCTTGGGACAGGTACGAGCAAGCCTGTGCGATGACGTTGT-----GGAAACGCTGAA 461
Db 13015 ArgArgGlyArgSerGlyProArgAlaGly-----CysAlaValAlaSerValArg 13031
Qy 460 TCATCGTGAGGAGTAGAGAGAGGTGATGAGCTCGCGG-----TGCCCTCAG 413
Db 13032 ArgThrArgProProArgArgValArgProAlaSerArgGlySerSerAlaArgProArg 13051
Qy 412 GGGCGCAAAATTGGCAAGCGTCGCGCT-----CCAGCACCTGACATCTCT--- 368
Db 13052 GlyAlaGlyThrAlaAlaArgThrProGlyGlyArgProArgProArgSerArgArg 13071
Qy 367 -----TCCAGGCCCTTGG 356
Db 13072 ArgAlaAlaProGlyCysAlaGlySerProProSerThrArgArgArgSerProTrp 13091
Qy 355 CCT-----TCGCGCTTCT-----TCTTGSCCA----- 335
Db 13092 ProAlaGlyProArgAlaProSerCysArgAlaAlaCysAlaValArgTrpAspSerAla 13111
Qy 334 -----CCTCGCACAGCG-----AGTGGCACAGGTGCGACCA 305
Db 13112 ArgArgArgProArgAlaAlaGlyArgAlaGlyGlyProCysAlaGlyCysGlyArgPro 13131
Qy 304 CGT----- 302
Db 13132 ArgArgArgProAlaValArgProAlaProArgSerSerSerGlyArgArgProSer 13151
Qy 301 -----AGATGGACTTGAACCTCGCCAGGTGCGATGTAAT 269
Db 13152 ArgProArgArgGlyHisArgArgSerArgTrpThr---SerSerArgThrArgTrpPro 13170
Qy 268 CAGCCATCATATCGACATCTCTCCCGCAGTGC----- 239
Db 13171 ArgProPro---ArgHisCysProArgAlaAlaAlaArgArgProArgArgAlaAspPro 13189
Qy 238 -----CACCAACCGGTCAACCCAGATGAGGTTCGAGC-----GCTCGGCCAGGC 194
Db 13190 SerProSerArgHisAlaProArgProArgAlaAlaAlaAlaThrTyArgSerAla 13209
Qy 193 GGGCAGCAAGGACGCGCGCTGGGGCCGTAGAGCTCTCCAGCGCAGCAGCGTATCAT 134
Db 13210 GlyProArgArgSerArgSerAlaProArgArg-----ArgArgArgSerHis 13226
Qy 133 CGCCCTTCT-----TGTGCCGAACCCACA 110
Db 13227 ArgProSerGlyArgArgArgAlaArgProValThrAlaThrAlaArgAla 13246
Qy 109 TATGGCGCAGNACGG-----TCAGGT-----CATCCTTCATGCTGCTGAGCTTGA 65
Db 13247 ArgAlaAlaSerArgSerTrpSerGlyArgArgArgProArgCys----- 13262
Qy 64 GCTTCTCCAGGAGAAAGTTCTTCTGTGTAGCTCGCAGCGCGCGCTCAGACCCGACC 5
Db 13263 -----GlyArgProProAlaAlaSerAlaGlyAlaArgThrArgSerProProThr 13279
Qy 4 CCA 2
Db 13280 Pro 13280
RESULT 5
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
```

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; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 19723
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 1,95e-19 Length: 19723
Score: 459.00 Matches: 241
Percent Similarity: 30.8% Conservative: 48
Best Local Similarity: 25.7% Mismatches: 271
Query Match: 12.7% Indels: 378
DB: 4 Gaps: 50

US-10-620-914-44 (1-1947) x US-10-084-846A-5 (1-19723)

QY 32 GCTACACCAAGAAGAACTTCTCCCTGGAGAGCTCAAGCTCAGCAGCATGAAGATGACC 91
Db 6473 AlaArgProArgGlyValAlaArgTrpArgTrpSer-----6484

QY 92 TGACCGTTCTCGCCCATATGTGGTTTCG-----GCAGCAAGAAGGGCGATGATC 139
Db 6485 -----ValCysProSerThrArgProProSerGlySerArgAlaMet---6498

QY 140 ACGTGTCTGCGTGGAGAGCTTCTACGGGCCCCAGG-----CGCTGCCTTTGCTG 190
Db 6499 -----ThrArgTrpSerArgProSerArgProArgArgProProSerProValThr 6516

QY 191 CCCGCTGGCCGAGCGCTCGAACCTCATCTCGGTTGACCTGGGTGGTGGCGACTGGGAGA 250
Db 6517 ProAlaArgSerArgSerSerAlaAlaGlyProThrArgGlyTrpSerTyrGlyGly 6536

QY 251 ATGTGATATGATGCTGATTACATCGACCTGGCGAAGTTCAAGTCCATCTACGTGGTCG 310
Db 6537 Ser-----ProProThrTrpProSerThrAla---ArgThrTrpThr 6549

QY 311 ACCTGTGCCACTCGCTGTGAGGTGGCCA-----340
Db 6550 ProCysSerThrGlyCysAlaArgProProThrSerValProAlaHisArgThrArgArg 6569

QY 341 -----AGAGAAGCGGAGCCAGGCTGGAGA-----ATGTCCAGTCTGTGAGG 388
Db 6570 SerThrArgArgSerArgThrArgGlyProArgProProThrAlaArgThrGlyArg 6589

QY 389 CCGACGCTTGGCAATTTC-----CGCCCTCGAGGGCAGCGACGCTCATCCTCTCT 442
Db 6590 ArgThrCysAlaThrArgCysGlySerProProArgSerProArgSerProArgThrAla 6609

QY 443 CCTACTCGCTCAGCATGATTCACCGTTCCACACGTCATCAGCAGCGCTTGTCTGTTACC 502
Db 6610 ThrGlyArgSerSerCysProArgThrProTrpSerArgThrArgSerThrArgArg 6629

QY 503 TGTCCCAAGACGGCTCG-----520
Db 6630 TrpProAlaAlaAlaTrpArgThrCysSerSerAspArgArgTyrGlyAlaThrSerPro 6649

QY 521 -----TGGCGTTGCGGCTTCTACGTGAGCG-----547
Db 6650 ArgProGlyProSerAlaProProTrpAlaProProThrAlaThrAlaAlaTrpThrGly 6669

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QY 548 -----GCAAGTACGACCTGCGCCCTGCGCCAGATGCGCTGTGTCGCCCGCTT 592
Db 6670 ArgArgSerSerArgThrGlyThrSerLysSerCysArgProThrProGlySerThrAla 6689

QY 593 TCTTCTGCG-----CATCGATCTTCGACATCGACACACATTGATCATCG 634
Db 6690 ArgCysGlyValProSerProGlyArgGluArgProSerAlaAlaThrThrSerThr---6708

QY 635 GCCCGAGCGCGCGCTTACCTGAGCAGAGAGCTGGAGCGGTGTGGAGCAGAGAACACCC 694
Db 6709 -----ProThr-----ArgCysTrpAlaArgProAla 6717

QY 695 AGGTTTCGATCCCTACGTGCGGTGGTGGCGGCCCTACTACTAGCTGTGGATTGCGCGCC 754
Db 6718 AlaSerArgAlaAlaThrCys---GlyCysGlyThrAlaAlaArgTrpThrThrAlaAla 6736

QY 755 TGCCAGCGTTGGCCAGCCCTCGACAGAGGACGCGTGGAGCGCGGCCCGCCATGTTCCCGC 814
Db 6737 ArgThrArgAlaAlaThrProSerThr-----AlaTrpArgSer-----SerArg 6751

QY 815 CCACCTTCTCTACACGCGAGTCGTGGAGGdACCCCGAGCCGGATATGAGGTGTGTGAGA 874
Db 6752 ProPro---CysTrpArgSerArgSer-----TrpArg 6761

QY 875 TCAACCCCAAGACACGGTGTGACCTGACCTGACGGCGGTGCATGCCCTCGAACCTGC 934
Db 6762 ProAlaProArgAlaLysSer-----AlaAlaProSerArgThrArgProThr 6777

QY 935 TGGTGCAGG-----GGCCCGGCCAGGTGTGTCGTTG 967
Db 6778 ArgCysArgArgValSerGlySerArgSerSerAlaAlaArgAlaArgTrpCysGlyTrp 6797

QY 968 -----ACTGCAACCCCG-----979
Db 6798 ProProGlyArgSerArgThrProProThrArgThrProProGlySerSerMetProArg 6817

QY 980 -----CGCAGTCGCGC-----991
Db 6818 ProGlyArgProArgArgThrSerProValTrpArgArgGlyArgCysTrpThrArgAla 6837

QY 992 -----TTCTGGAGCTCAAGAGGTGGCCATTGAGCAGC 1024
Db 6838 SerThrGlySerAsnArgProThrProAlaTrpSerProGlyGlyTrpPro-----Arg 6855

QY 1025 TGGAGTTTGAGAGCGTGTGGCAGCTGTTCDGCGAGGCG---TGCACCCGCGCATTTAGG 1081
Db 6856 TrpAlaTrpProArgProValSerIleGlyAlaSerSerArgCysProProValSerVal 6875

QY 1082 AGCTGTACGAGAGAAGCTGGCGCCCTTCTGTGCGAAACACGACACAACTTCTGTGTCCA 1141
Db 6876 TyrCysThrLeuArg-----CysSerArgProThrProArgProGlyPro 6890

QY 1142 AGCGCTCTGTGTTCTCCAGCAGCGCTGTACTACCAGG-----GCGGCATGGCAGC 1195
Db 6891 ArgCys-----TrpThrProCysArgSerArgArgProProSerTrpAlaSer 6906

QY 1196 TGTCTGGTGTGCTGAGTGTGCGCTGCGTGGGACTGGGCAAGACCGCTCAAGC---1252
Db 6907 ArgSer-----SerAlaTrpSer---CysThrSerThrArgSerProSerThrAla 6922

QY 1253 -----GCTCGCCCAAGC-----1264
Db 6923 ArgHisArgArgArgArgSerArgSerArgSerIleProAlaSerProThrProCys 6942

QY 1265 -----CGCCCAATGGAGGACGCGCGCTGTGGGACA 1300
Db 6943 ThrProTrpSerArgThrGlyArgAspAlaArgTrpArgAlaCysAlaAlaCysAlaThr 6962

QY 1301 GCAACATGCTCATCCATCTCGTGAAGAACGCGGCCCAAGCGCG-----1342
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QY 1343 ---TGGTGT-----GGCTGTGTCG-----1357

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6983	Db	ThrTrpCysArgSerArgValCysArgArgSerCysValProGlyCysSerThrArg	7002
1358	Qy	-----TCAAGTTTCGTGAGCTGGTGTCTTCA-----ACAAGGCGGTCTCTGT-----	1399
7003	Db	CysAlaSerArgSerArgArgCysAspSerProProArgProCysThrPheAlaAla	7022
1400	Qy	-----GGTTCCGCGCGCGTCCCGGCAAGC	1426
7023	Db	ArgTrpTrpSerArgGlySerThrArgArgTrpTrpSerAlaAlaGlyTrpArgSerAla	7042
1427	Qy	AGTACGGCGTGATCAAGCGGACGGCATCC-----CCATTGAACAATTACATCG	1474
7043	Db	SerAlaGlyThrCysArgProThrSerSerGlySerCysProProSerAlaThrSerSer	7062
1475	Qy	CGCGCACCA-----TGGACGGCGTGGCGGAGAACTCCGACGTGCGCAAGCAGAACT	1525
7063	Db	IleThrProAsnAlaSerArgAsnThrArgArgArgThrAlaMetArgProGluArgThr	7082
1526	Qy	ACTTCTACTACAACTGCCTCACCGGCAAGTTCTCGCGCAAACTGCCCACT-----	1579
7083	Db	AspSerValThrHisValSerArgGlyArgGlyGluArgAlaAlaProAlaGlyPro	7102
1580	Qy	-----ACCTGCGGAGGCGCGCTTCGCCA	1603
7103	Db	GluThrGlyLysProGluLysHisAlaSerThrIleValValGlyArgArgHisSerMet	7122
1604	Qy	CCCTCA-----	1609
7123	Db	ProSerGlyValProLeuLysArgProAspLeuThrAlaLeuThrAlaArgCysGlyIle	7142
1610	Qy	---AGAGTGGCGTGTGGCAACACTGACCGTCTCCACAACTTCTTCATGGAGGAGCTCA	1666
7143	Db	ArgArgSerTyrrTrpTrp-----AlaGlyLeuAlaArgGlyCys	7155
1667	Qy	AAGCGCGCACTACACAAGGTGATTCGTATGACACACAGTGG-----	1708
7156	Db	GlyArgLeuArgIleProArgProAsnAsnTrpSerArgTrpProIleGluLeuPheSer	7175
1709	Qy	---ACTGGCTGGATA-----	1720
7176	Db	ProMetTyrrTrpIleProSerArgArgProGluTyrrArgArgSerGlyLeuSerSerGly	7195
1721	Qy	-----TGCCCGTGCCCAACGAGCTGGCGGAGTGCCTGCGCCAAAGC	1759
7196	Db	ArgProArgArgSerArgLeuProTrpGluThrAlaArgSerSerAlaTrpThrSer	7215
1760	Qy	AGTTGGCGCGGGCGGATCGTATCTGGCGCTCCGCTCCCTCAGCCCGCCCTACGCCG	1819
7216	Db	ProThrSerSerArgThrProArgAlaGlyTrpProThrProCysSerCysProValThr	7235
1820	Qy	AGCTGATCCAGAGCGGGCTTCGACCTGC-----	1849
7236	Db	Ser---SerAlaThrThrThrSerSerCysThrTrpAlaThrThrThrSerTrpThrAla	7254
1850	Qy	-----GTCGATCCCGCGCCACTCAGG-----	1873
7255	Db	SerSerThrSerTrpArgThrSerAlaAlaThrSerProProArgArgSerCysSerPro	7274
1873	Qy	-----	1873
7275	Db	GlySerProThrArgAlaGlySerAlaTrpProAsnLeuThrArgThrAlaGlyProArg	7294
1874	Qy	-----GCTACATGGACCGCGTCAACATCTGACA-----	1900
7295	Db	SerTrpArgSerProArgThrProGlyValaThrTrpArgSerSerAlaCysThrProSer	7314
1901	Qy	---GCTCCTCTTACA-----TGCCCGCGCGGAAGGGCGGCAAGAGCAACT	1945
7315	Db	AlaArgProCysThrArgProTrpProAlaSerGlyValArgProGlyGlyThrSer	7332

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; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084.846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 19723
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 2,41e-19 Length: 19723
Score: 457.50 Matches: 242
Percent Similarity: 33.1% Conservative: 46
Best Local Similarity: 27.8% Mismatches: 256
Query Match: 12.6% Indels: 325
DB: 4 Gaps: 55

US-10-620-914-44 (1-1947) x US-10-084-846A-5 (1-19723)
Qy 1945 AGTTGTCTCTTCGTGGCGCCCTTCGGCGGCATGTAGA----- 1907
Db 6222 SerThrSerGlyTrpArgPro-----GlyProCysArgGlyProSerValArgThrPro 6239
Qy 1906 -----AGGAGCTGTACATGTTGACGGGTCCATGTAGC-----CCT 1871
Db 6240 AlaGlyArgLeuCys-----ProValSerAlaThrAlaAlaProTrpPro 6254
Qy 1870 GAGTGGCGCGCGGATGCAGCGCAGCTCGAAGCCGCGCTTCTGGATCAGCTCGGCGTAGG 1811
Db 6255 MetTrp-----SerSerAsnArgArgProProArgProProAlaProArgArg 6270
Qy 1810 GCGGGCTGAGGAGCGGAGCGCCAGTACGATGCCCGCGCGCAACCTGCTTGGCCA 1751
Db 6271 Ser-----ArgPro-----GluProCysSerArg 6278
Qy 1750 GGCACTGGCGAGCTCGTTGGCCACGGGCATATCCAGCCAGTCCACGTGGTCCATCAGAA 1691
Db 6279 CysProArgProProArg-----ArgArgSerValThrAlaArgProArgSerProSerGly 6297
Qy 1690 TCACCTTTGGTGTAGTGCGCGCTTTGAGCTCCTCCATGAAGAAGTTGTTGGAGACGGTCA 1631
Db 6298 Ser-----ArgArgAlaLeu-----ThrTrpProArgSer 6307
Qy 1630 GGTGTGCA-----CCAGCCACTCTTGAGGG-----TGGCGAAGG 1595
Db 6308 GlyThrProTrpProLeGlySerProArgTrpSerThrGlyArgProSerTrpArgPro 6327
Qy 1594 -----CCGCTTCGGCGAGTAGTGGGGC----- 1571
Db 6328 AlaGlyThrAsnTrpProProGlyCysAlaArgTrpProLeuArgAsnProArgProVal 6347
Qy 1570 AGTTGTGCGCAGGAACTTGGCGGTGAGCGAGTGTGTAGTAGAGTAGTCTCTCTTGGCCA 1511
Db 6348 SerSerProGlyProArgCysArg-----MetProAlaValProSerGlyCysSer 6364
Qy 1510 CGTGGAGTTCCTCGCCACGCGCTCCATGTTGCGCGCATGT----- 1469

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US-10-620-914-44 (1-1947) x US-10-084-846A-8 (1-19608)

QY	17	ACGCCCGC-----CTGCGAGCTACACCAAGAAGAACTTCTCCCTGGAGAAGCTCA	67
Db	5039	ThrAlaGlyArgThrProLeuArgArgAlaProArgGlyThrHisPro-----	5054
QY	68	AGCTCAGCAGCATGAAGGATGACCTGACCGTTCTGCGCCATATGTGGTTCGCGACGAAGA	127
Db	5055	-----AlaSerGlySerArgArgArg	5061
QY	128	AGGCGATGATCAGCTGCTGCTGAGAGCTTCTACGGGCCCCAGCGCGCTGCCTTTG	187
Db	5062	ArgSerSerGlnValArgLeuGlyGlnTyAlaGlySerHisAlaPro-----	5078
QY	188	CTGCCCGCTGGCGGCGAGCTCGAACCTCATCTGGGTTGACCTGGGTGGTGCA-----	241
Db	5079	LeuGlnAspGlyArgGlyAlaAcgHisSerArgSerGlyCysTyxIleValAlaHisGlu	5098
QY	242	-----CTGGGAGATGTCGATATGATGGCTG	268
Db	5099	GluGlyLeuGluIleProLeuGluArgAspTyThrArgArgSerIleSerGlnLeu	5118
QY	269	-----ATTACATCGACTCG	283
Db	5119	ProValProAspValHisPheTyProGlnCysAlaAlaThrAsnLeuAsnTyGlnTyr	5138
QY	284	CGAAGTTCAAGTCCATCTACGTGCTGCACCTGTGCCACTCGCTGTGCGAGGTGGCCAAGA	343
Db	5139	GlyAlaProCysProIlysIysCysSerSerAlaValGlyArg-----ArgAspProArg	5156
QY	344	AGAAGCGAAGGCCAAGGCTGGAAGAATGTCAGTCTGTGG-----AGGCCGAGCTT	397
Db	5157	ArgProProCysSerAlaArgProAlaCysProSerTyTrpAsnGlyArgProSerArg	5176
QY	398	GCCAAATTGGCCCCCTGAGGCGACCGCGCTCATCCTCTCTCTACTCGCTCACGA	457
Db	5177	AlaThrThrSerAlaSerArgSerProProArgAlaAlaProSerSerThrSerSerAla	5196
QY	458	TGATTCCACCGTTCCACAACGTCATCGACGAGCTTGTCTGTACTGTGCCAAGCGGC	517
Db	5197	ArgTrpArgArgSerThrProAlaValThrArgSerArgThrAlaCys-----	5212
QY	518	TGTTGGCGTTGCGGACTTCTACGTGAGCGGCAAGTACGACCTGCGCCCTGCGCGCAGATGC	577
Db	5213	-----CysCysAlaGlyAlaArgArg	5219
QY	578	CCTGTTGCGCGCTTCTTCTGCGATCGATCTTCGACATCGACATATGATCATCGGCC	637
Db	5220	ThrGlyArg-----SerThrGlyArgArgSerSerValPro-----ThrSerAla	5234
QY	638	CCG-----AGCGCCGCGCTACTGGAGCAGAAGCTGGAGCGCGTGGGAGCAGAACA	691
Db	5235	ProGlyArgSerThrAlaThrThr-----SerThrThrCysSerArgThr	5249
QY	692	CCGAGGTTTCGAPCCCTACGTGCGCGTGGTGGCGCGCCCTTACTACGTGTGGATGGCC	751
Db	5250	ArgSerSerArgAlaProThr-----SerProArgAlaSerArgSerSerAla	5265
QY	752	GCTTGCCACGTTGGCCACGCCCTCCACAGAGCGCGTGGAGCGCGCCCATGTTCC	811
Db	5266	CysCysSerThrAlaThrAlaArgLeuGlyArgSerGlyTrpThrProThrProValSer	5285
QY	812	CGCCACCTTCTGTACACGCGAGTCGTGGGAGGACCCCGAGCGCGGATATGGAGGTGATGG	871
Db	5286	-----TrpSerAlaArgSerSerThrThrSer-----	5294
QY	872	AGATCAACCCAAAGGACAGGTGCTGACCTGACTAGCGCGCGTGCMAATGCCCTGAACC	931
Db	5295	---SerThrProArgAla-----	5299
QY	932	TGCTGTGTCAGGGCGCGGCCAGGTGGTGTGGTGGACTGCAACCCCGCGCAGTGGCGC	991
Db	5300	-----GlyProAla-----SerSerProSerThrArgThr	5309

Alignment Scores:		
Prod. No.:	1.23e-18	Length: 19609
Score:	446.00	Matches: 205
Percent Similarity:	37.5%	Conservative: 57
Best Local Similarity:	29.4%	Mismatches: 248
Query Match:	12.3%	Indels: 188
DB:	4	Gaps: 34

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Qy 992 TTCCTGGAGCTGAAGAAGTGGCCATTGAGAGCTGGAGTTTGAGGACGTGTGGCAGCTGT 1051
Db 5310 -----AlaAlaArgThrArgSerSerAla 5317
Qy 1052 TCGCGGAGG-----GGCTGACCCGGCGCATTTAGGAGCTGTACGAGAAGAGCTGGCGC 1105
Db 5318 ThrSerArgSerGlyAlaThrGlyArgAlaAlaArgCysProValArgProGlnGly 5337
Qy 1106 CTTCTGCTGCGCAACACGACCAACTCTGGTCCA-----AGCGCCTCTGGT 1153
Db 5338 AlaSerThrSerSerAlaProArgThrAlaGlyThrGlySerArgCysAlaGlyThrGly 5357
Qy 1154 ACTTCCAGCAGCGCTGTACTACGAGGGCGCATGGGCAAGCTGTGGTGTGTGAGT 1213
Db 5358 ThrAlaSerValSerSerAlaThrArgThrGlySerTrpSerAlaAlaGlyAsnThrPro 5377
Qy 1214 GCCTGGCGGTGGTGTGGGAC---TGGGCAAGACCGTCAAGCGCTCGCCAAACGCGCCA 1270
Db 5378 ThrTrpArgArgCysTrpProArgTrpSerArg-----AsnProArgProCysAlaThr 5395
Qy 1271 CAATGGAGGACAGCGCGTCTGTGGGACAGCAATGCTCATCCACTTCTGTGAAGAAG 1330
Db 5396 SerTrpArgThrAlaSerThrSerArgAlaTyrglyTrpSerArgThrSer---ProThr 5414
Qy 1331 GGCCCAAGCCGCTGGTGTGGCTGTTCGTCAGTTGCTGAGCCTGG-----TGCTCTTCA 1384
Db 5415 SerProThrAlaSerThrAlaProAlaThrThrSerProAlaThrProProAlaSerSer 5434
Qy 1385 ACAAGGCGGTCTGTGGTTCGGCGCGCGGTGGCGGCAAGCAGTACGCGTGTATCAAGG 1444
Db 5435 ThrArg---CysCysProAlaSerThrTrpArgSerThrAlaAlaCysTrpProArg 5453
Qy 1445 CGGACGGCATCCCATTTAGAACTACATTCGCGCGCACCATGGACGGCGTGGCGGAGAACT 1504
Db 5454 ArgProCysSerProArgThrArgThrSerArg-----5464
Qy 1505 GCGAGTGGCGCAAGCAGACTTCTTACTACAACTGCTCACCGGCAAGTTCCTGCGCG 1564
Db 5465 ArgArgArgProGlyArgSerThrSerArgSerThrAlaThrProThrSerGlyCysSer 5484
Qy 1565 ACAACTGCCACCTACCTGCGGAGGCGGCTTCGCCACCTCAAGAGTGGCGTGTGGT 1624
Db 5485 ProTrpCysProAlaCysThrSerAsnArgProAlaArgProProThrSerSerTrpPro 5504
Qy 1625 ACA-----ACCTGACCTCTCCACAACTTCTTCATGGAGAGCTCAAAGCGGCA 1675
Db 5505 ThrArgProArgSerAlaProArgProSerThrSer-----ArgSerThrAlaArgTrp 5522
Qy 1676 CTTACACCAAGGTATCTGATGACCAACGCTGGACTGGCTGGATATGCCCGTGGCCACG 1735
Db 5523 SerProPro-----AsnTrpSerArgAspTrpProThr 5533
Qy 1736 AGC---TGGCCGAGTGCCTGCGCAAGCAGGTGTGGCGGGCGCATCG---TCATCTGGC 1789
Db 5534 SerThrThrProSer-----ProAlaArgThrArgThrAlaProSerArgArgThrPro 5551
Qy 1790 GCTCGGCTCCTCAGCGCGGCTTACGCGGAGCTGATCC-----1828
Db 5552 ArgProThrProCysArgArgThrThrProSerAlaSerCysSerArgArgProArgThr 5571
Qy 1829 -----AGAAGCGGGCTTCAGCGTGGCTGCATCCGCGCGCCACCTCAGGCTACATGG 1882
Db 5572 ProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeuProAlaArgTrp 5591
Qy 1883 ACCGGTCAACATGTACAGCTCTCT-----TCTACATGGCGCGCGGGAAGG 1927
Db 5592 ThrProThrThrSerThrThrProProArgValSerThrTrpProAlaArgArg 5609

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RESULT 9

US-10-084-846A-3

; Sequence 3, Application US/10084846A

; Publication No. US2004000626A1

GENERAL INFORMATION:

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; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

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Alignment Scores:

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Pred. No.: 1,75e-18 Length: 19695
Score: 443.50 Matches: 229
Percent Similarity: 34.3% Conservative: 48
Best Local Similarity: 28.4% Mismatches: 213
Query Match: 12.3% Indels: 317
DB: 4 Gaps: 51

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US-10-620-914-44 (1-1947) x US-10-084-846A-3 (1-19695)

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Qy 23 GGCCTGCGAGCTACA-----CCAAGAAG-----ACTTCTCCCTGGAGAGCTCAAGC 70
Db 8455 GlyGluArgThrHisProArgArgHisTrpThrGlyProArgArgSerSerGly 8474
Qy 71 TCAGCAGCATGAGGATGACCTGACCCGTTCTGCCCATATGTGTTCCGCGAGCAAGAGG 130
Db 8475 SerAsp-----GlyThrAlaSerArgThr 8482
Qy 131 GCGATGATCACGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGG-----CCGCTG 181
Db 8483 -----ArgAlaArgPheSerProArgThrArgSerProVal 8494
Qy 182 -----CCTTGTGTCGCGCTGGCGAGCGCTCGAACC 214
Db 8495 SerArgArgAlaProAsnGlySerSerProAlaSerProThrArgAlaCysAlaProThr 8514
Qy 215 TCATCTGGTTGACCTGGTGGTGGCTGGGAGATGTCGATGATGCTGATTACA 274
Db 8515 ThrThrGly-----Thr 8518
Qy 275 TCGACCTGGCGAAGTTCAAGT---CCATCTACGTGGTGCACCTGTGCCACTCGCTGTGCG 331
Db 8519 SerProSerArgAlaMetSerValProSer-----SerThrAlaCysThr 8533
Qy 332 AGGTGGCCAAAGAGCGGAGCCAGGGCTGGAGA-----ATGTCAGGTCTGTGG 385
Db 8534 ThrTrp---ArgSerArgThrGlyProArgAsnGlyThrCysCysThrAlaArgAsnTrp 8552
Qy 386 AGGCGGACGCTTGGCAATTTGCGCCCTCGAGGGCACCGGAGCGCTCATACCTTCTCT 445
Db 8553 ArgSerSer-----ProProArgSerTrpThrAlaArgSerCysProProPro 8568
Qy 446 ACTCGCTCA-----CGATGATTCCACCGTTCCAAACGTC 481
Db 8569 ThrArgSerSerArgSerArgThrGlyProArgArgCysHisGlyThrValThrAla 8588
Qy 482 TCGACCAAGGCTT---GCTCGTACTGTCCCAAGACGCGCTGTGGCGGTTCGCCACTTCT 538
Db 8589 SerThrSerAlaArgAlaArgSerAlaAlaSerAlaTrp-----8602

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QY 539 ACGTGAGCGGCAAGTACGACCTGCGCCCTGCGCCAGATGCCCTGGTCGCGCCGTTTCTTCT 598
Db 8603 -----ThrThr-----ProAspArgThrThrAspAla 8611
QY 599 -----GGCGATCGATCTTCGACATCGACACCAATTCACATCGCGCCCGAGCGCC 646
Db 8612 TrpArgArgPheArgAspArgThrCysSerProThrThrProArgTrpArgArgCysAla 8631
QY 647 GGCCTC---ACCTGAGCAGAGCTGGAGCGG-----TGT 679
Db 8632 ArgProAspProTIPheArgSerArgSerAlaArgAlaThrTIPheCysThrThrSer 8651
QY 680 GGGACGAGAACCCAGGTTTCATCCCTAGTCCGCTGGC----- 721
Db 8652 GlySerSerThrValArgAlaArgThrProThrAlaValGlyGlyProSerSerSer 8671
QY 721 ----- 721
Db 8672 SerThrProThrArgProHisArgArgArgProGluArgCysAlaAlaGluArgGlnAla 8691
QY 722 -----TGCGCGCCCTCCT----- 733
Db 8692 AspileGluArgGlnValArgGluSerPheGlyGlyLeuCysSerProProArgThrGly 8711
QY 734 -----ACTAGCTGGATTGGCCGCTGCCAGCGTTGGCCACGCC---TGCAAGAGG 784
Db 8712 ArgAspileThrCysAlaTIPheCysProTIPheCysAlaProArgAspThrArg 8731
QY 785 AGCGGTGG-----AGCGCGCGCCATGTTCGCGCCA 817
Db 8732 SerGlyTIPheArgAlaArgArgArgAsnAlaGlySerProArgProAlaCysArgSer 8751
QY 818 CCTTCCTGTACACGCGAGTCGTGGAGAGACCCGAGCCGATATGAGGTGTGAGATCA 877
Db 8752 ArgCysSerThrArgArgThrTIPheAlaProGly-----TIPheArgSer 8766
QY 878 ACCCAAGGACACGGTGTGACCTGTAGCGCGCTGCAATGCCCTGAACCTGTGTGG 937
Db 8767 -----MetCysArgPro----- 8770
QY 938 TGC-----AGGGGCGCGCCAGGTGG---TGTCGTGGACTGCAACCCCGCGAGT 985
Db 8771 CysThrHisArgArgSerProValArgGlyArgCysArgCysThrArgSerProGlySer 8790
QY 986 CGGCGCTTCTGGAGCTGAAGAGGTGGCCATTACAGCAGCTGGAGTTTGAGGACGTGTGGC 1045
Db 8791 Arg-----CysSerArgSerThrThr 8797
QY 1046 AGCTGTTCGGCAGGGCGTGCACCGCGCATTTGAGAGCTGTACGAGAGAAGCTGGCGC 1105
Db 8798 SerThrProAlaThrCysAlaThrSerGlyArgSerArgSerThrArgCysSerAlaAla 8817
QY 1106 CTTTCCTGTCCCAACACGACCACTTCTGGTCCAAGCGCTCTGGTACTTCCAGCAGC 1165
Db 8818 MetThrThrArgAlaSerAlaThrThrGlyGlyPro-----ThrTIPheCysThrThr 8835
QY 1166 GCCTGTACTACAGGGCGCATGGCAAGCTGTGCTGGTGTCTGCAAGTCTGGCGCGTGG 1225
Db 8836 SerTrpProSerArgAlaHisTIPheSerProArgSerGlyAlaCysArgAla----- 8852
QY 1226 TGCTGGGACTGGCAAGACCGTCAAGCGCTCGCAACCGCCGCCAAC----- 1273
Db 8853 -----SerMetCysArgProGlySerSerAlaProTIPheArgProSerArgGlySerThr 8870
QY 1274 TGG-----AGGAGCAGCGCGTCTGGCAACCGCCGCCAAC----- 1306
Db 8871 TrpSerArgThrArgCysArgAlaSerArgSerThrAlaSerSerGlyAlaAlaThr 8890
QY 1307 TGCTCATCACTTCGTGAAGAACGGGCCA-----AGCGGTGG--- 1345
Db 8891 GlySerSerThr-----ArgTrpThrProHisArgThrTrpArgCysArgArgTIPheAla 8908

QY 1346 -----TGTCGCTGTTCGTCAGTTCTGTGAGCGCTGCTCTTCAACAAGCGCG----- 1393
Db 8909 ThrArgCysGlyCysProCys-----AlaThrCysProThrThrAlaProArgAla 8925
QY 1394 -----TGCTGTGGTTTCGCGCGCGCGTGC 1417
Db 8926 ArgThrArgGlySerTrpGlyArgSerGlyAlaAlaAlaCysAlaSerSerGlyAlaThr 8945
QY 1418 -----CGGCAAGCAGTACCGCTGTATCAAGCGGAGCGCATCCCCA---TTGAGAACT 1468
Db 8946 ArgProArgAlaSerSerAlaProThrTrpArgArgCysGlyThrProSerThrArgArg 8965
QY 1469 ACATCGCGCGCA-----CCATGACGCGGTGGCGG 1498
Db 8966 CysGlyArgAlaAlaArgTrpCysSerArgArgArgArgAsnArgTrpArgSerTrpGlu 8985
QY 1499 AGAATCGCACGTGGCGAAGCAGAACTACTTCTACTCAACTGCCTCACCGSCAAGTTCC 1558
Db 8986 ArgCysArg-----ProAlaSerGly 8992
QY 1559 TGCAGCAACTGCCCCACCTACCTGCGCGAGGCGCTTCGCCACCCCTCAAGAGTGGCG 1618
Db 8993 CysCysAlaThrAla-----ArgTrpSerSerSerSerArgThrAla 9006
QY 1619 -----TGGTGGACAACC---TGACCGTCTCCACCACTTCTCATGGAGGAGCTCAAAG 1669
Db 9007 ThrCysTrpCysThrThrAlaAlaProThrAlaThrThrAlaSerTrpArgGlyPheArg 9026
QY 1670 CGCGCACCTACCAAGGTGATTCTGATGGACCACTGGACTGGCTGGATATGCCCGTGG 1729
Db 9027 SerCysProSerProSer-----ThrThr----- 9034
QY 1730 CCAACGAGCTGGCGAGTGCCTGGCCAAAGCAGAGTTTGGCCCGGCGGCACTCGTCACTCGC 1789
Db 9035 -----ThrArgSerAlaAlaAlaValSerIleProPro 9045
QY 1790 GCTCGGCT-----CCCTAGCGCGCTAGCGGAGCTGATCCAGAGGCGGCTTCG 1843
Db 9046 AlaProProCysProAlaLeuArgProArgProArgArgSerArgArgCysAla 9065
QY 1844 ACGTGC-----GCTGCATCCGCGCGCCACTCAGGGGTACATGACCGCGTCAACA 1894
Db 9066 GlyCysCysSerThrThrAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 9085
QY 1895 -----TGTCAGCTCCTTCTTACATGGCCCGCGCGA 1924
Db 9086 GlyHisLeuArgProProArgSerProGlyCys-----ProAlaSerTrpArgThrAla 9103
QY 1925 AGGCGCGCAAGAGCAACT 1945
Db 9104 GlyCysArgArgArgThrSer 9110
RESULT 10
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608

; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

Alignment Scores:
Pred. No.: 5,05e-18 Length: 19608
Score: 436.00 Matches: 217
Percent Similarity: 35.0% Conservative: 40
Best Local Similarity: 29.6% Mismatches: 237
Query Match: 12.0% Indels: 240
DB: 4 Gaps: 44

US-10-620-914-44 (1-1947) x US-10-084-846A-8 (1-19608)

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QY 1939 CTTCTTGGCGCCCTTCGGCGGGCCATGTAGAGGAGCTGTACATGTTGACGGGTCCA 1880
Db 10543 ProArgThrArg-----CysProArg----- 10549
QY 1879 TGTAGCCGTAGTGGCGCGGATGACAGCGCAGCTCGAAGCCCGCTTCTGGATCAGCT 1820
Db 10350 -----ProArgArgProSerProThrAlaArgArgProProArgGlyGlySerAla 10567
QY 1819 CGGCGTAGGGCGGTGAGGAGGCGGAGCCAGATCAGCATCGCCCGCGCCCACT 1760
Db 10568 AlaArgArgPro-----ArgArgAlaLysValProAlaArgArgProAlaValSer 10585
QY 1759 GTTGGCCAGGCACTCGGCCAGCTCGTTGGCCAGCGGCATATCAGCCAGTCCACGTGGT 1700
Db 10586 ProProProGlyGlySerGlyGlyArg-----ThrAlaProGlyAlaAlaProProArg 10603
QY 1699 CCATCAGAATCACTTGTGTAGTGGCGCTTTGAGCTCTCCATGATGAAGAAGTTGGTGG 1640
Db 10604 ProSerArg--ProTriProGln----- 10610
QY 1639 AGACGTCAGTTGTCCACACGCCCACTCTTGAGGGTGGCGAAGCCCGCTCGC---GCA 1593
Db 10611 GlyArgThrGlySer-----GlyTrpArgArgArgAspArgTrpGly 10624
QY 1582 GGTAGTGGGCGAGTTGTCGCGCAGGAACCTTGCCGGTGAGGCAGTTGTAGTAGAAGTAGT 1523
Db 10625 GlyArgArgSerAlaCysArgSerGly-----ArgGlyThr 10636
QY 1522 TCTGCTTGGCAGCTGGCGAGTTCTCCGCCAGCGCTCCATGGTGGCGCGATGTAGTTCT 1463
Db 10637 Ala-----AlaGluSerProProArg-----CysArgSerCysSerSer 10649
QY 1462 CAATGGGATGCGCTCCGCTTGATCAGCGGTACT-----GCT 1424
Db 10650 ---TrpArgCysArgglyAlaProAlaGlyArgSerThrGlyAlaProAlaGlySer 10668
QY 1423 TGCCGGCAGCGCGCGCGCAACACACAGCAGCGCTTGTGAAGAGCACCAGGCTCAGCA 1364
Db 10669 CysAlaAlaProGlyArgArgProAlaAlaLeuPro-----AlaPro----- 10682
QY 1363 ACTTGACGAACAGCCACACACAGCGCTTGGCGCGCTTCTTCCAGAAAGTGGATGACATGT 1304
Db 10683 -----ProProValProAlaAlaProAlaPro----- 10691
QY 1303 TGCTGTCCACAGAGCGGCTGCTCTCATTTGGGCGCGTGGCGAGCGCT----- 1250
Db 10692 -----ProProArgProAlaAlaProPro-----ArgArgTrpArgAlaAlaPro 10707
QY 1249 -----TGACGGTCTTGCCAGTCCAGCA---CCACGG----- 1220
Db 10708 ValArgArgArgArgArgCysProArgProSerCysProArgArgCysThrArgValCys 10727
QY 1219 CCAGGCACTGACGACCCAGCAGCTTGGCCATCGCCCTGTGGTAGTACAGCGCGTGT 1160
Db 10728 ProGly---SerAlaProAlaAlaThrGlyPro---ArgProGlyArgArgCysArgAla 10745
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QY 1159 GGAAGTACCAGAGCGCTTGGACCAGAAAGTTGTGGCTGTTTGGACAGGAGGCGCCA 1100
Db 10746 ArgSer-----AlaTrpAlaAlaAlaAlaArgArgPro 10756
QY 1099 GCTTCTTCTCGTACAGCTCTCAATGCGGGGTGCAGCCCTCCCGAACAGCTGCCACA 1040
Db 10757 Ala-----AlaAlaProProArgProValArgGly 10766
QY 1039 GTCCTCAAACTCCAGCTGTGAATGGCCACCTTCTTCAGCTCCAGAACGCCCACTCGC 980
Db 10767 ProProArgThrGlySerGlyArgGlyProThrArgArgArgThrSerArgSerThr 10786
QY 979 CGGGTTGTCAGTCCACGACACACACCTGGCGGCCCTCGCCACGACAGGTTTCAAGGCAT 920
Db 10787 AlaGly-----ProProArgProGlyArg-----AlaProAlaArgSerProArg 10801
QY 919 TGCAGCCGCGCTAGTACAGGCTCAGCCCGTGT---CCTTGGGTTGATCTCCA---TCA 866
Db 10802 CysArgThrArgAlaThrHisArgSerAlaArgProGlyAlaArgProValArg 10821
QY 865 CCTCATATCCGGCTCGGGTCTCCACGACTCGGTGTACAGAGGTGGCGGGAACA 806
Db 10822 ProArgArgProCysArgAlaProProGlyArgAlaAlaSerGlyArgArgSerPro 10841
QY 805 TGGCGCGCGCTCCACGCGCTCTCGTCGAGGCGTGCACCAACGCTGGGACGCGGCCAA 746
Db 10842 ArgCysHisSerCysAlaAlaProArgArgSerThrSerArgSerArgAlaGlyArg 10861
QY 745 TCCACACGTAGTAGGGGCGCGCAGCCACGACGTAGGGATCGAACCCCTGGGTGTCT 686
Db 10862 ArgArgArgSerArgAlaThrAlaSerAlaAlaArgThrGlyAlaAlaAlaAlaAla 10881
QY 685 GCTCCACACGCGCTCCAGCTTCTGCTCCAGGTAGGCGCGCGCTGGGCGCGATGTCAA 626
Db 10882 AspArgThrAlaAlaValCysThrTrpProAlaHisArgThrProAlaGlyArgPhePro 10901
QY 625 TGTGTGATGTCGAAGATCGATCGCCAGAAGAAACGCGCGCACAGG----- 578
Db 10902 SerCysProAlaArgArgAlaProGlyProAlaSerGlyArgSerArgArgProArgVal 10921
QY 577 -----GCATCTGGCGCA 566
Db 10922 ProAlaThrAlaGlyThrProProGlySerArgValProArgAlaAlaAlaProArgPro 10941
QY 565 GGGCGCAGCTGTAATCTCCGC-----TCAGTAGA-----AGTCGCAACGC 524
Db 10942 GlyAlaProCysThrCysAsnValProProSerSerArgArgThrSerSerSerSer 10961
QY 523 CCACCA-----GGCCGCTCTTGGGACAGGT 500
Db 10962 LeuProAspLeuProPheAspValCysLeuAlaLeuGlyAlaAlaLeuArgAlaPro 10981
QY 499 ACGAGCAAGCTGTGTCATGACGTTGTGGACCGTGAATCATCGTAGCGAGTAGGAGA 440
Db 10982 AlaValArgProGlyArg-----ArgThrArg 10990
QY 439 AGGTGATGACGCTCGCGTGC-----CCTCAGGGGCGCAAAATTGGCAAG 395
Db 10991 ArgTrpSerAlaAlaAsnCysArgTrpArgSerGlyProAsnArgGlyArgAlaGlyArg 11010
QY 394 CGTCGGCTCCA---CGACCTGGACATTTCTCCAGCCCTTGGCCTTCGCCT----- 347
Db 11011 ArgAlaProProArgArgProGly-----ProGlyProGluProArgValArg 11026
QY 346 -----TCTTTGCGCCACTCGCACGCGAGTGGCACAGT----- 311
Db 11027 SerArgAlaProSerProProArgArgArgGlyAlaGlyAlaAlaProGluProPro 11046
QY 310 -----CGACCAGTAGATGACT----- 293
Db 11047 ProGlyIleArgCysAlaValArgArgProGlyArgCysSerAspCysArgProCys 11066
QY 292 -----TGAACCTCGCCAGGT 278
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Db 11067 AlaGlyArgArgArgGlyHisGlyAlaMetalaProProArgProGlyThrAlaProGly 11086
QY 277 CGATGTAATCAGCCATCATATCGACATTCTCCAGTCCACACCCAGGTCAACCCAGA 218
Db 11087 ArgAlaArgArgArgTIPAlaArg-----ProGlyArgProArg 11099
QY 217 TGAGTTCCAGGGCTCGG-----CCAGCGGGCAGCAAGAGCAGCGGCTGGGCGCCGT 164
Db 11100 ThrArgArgArgAlaAlaProValProArgGlyAlaAlaGlyProValProGlyProSer 11119
QY 163 AGAGCTCTCCA-----GGCAGCAGCGTGAT---CATCGCCCT----- 128
Db 11120 ProAlaSerProSerCysAlaArgGlyArgGlyArgAspAlaHisArgProArgArgGly 11139
QY 127 ---TCTTCTGTCGCAACCATATATGCGCGCAGAACCGTCCAGGT 89
Db 11140 SerSerSerArgArgSerAlaGlyProArgArgSerGly 11153

RESULT 11

US-10-084-846A-4
; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLWENEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4

Alignment Scores:
Pred. No.: 2,77e-17 Length: 19725
Score: 424.00 Matches: 222
Percent Similarity: 33.2% Conservative: 41
Best Local Similarity: 28.0% Mismatches: 251
Query Match: 11.7% Indels: 278
DB: 4 Gaps: 49

US-10-620-914-44 (1-1947) x US-10-084-846A-4 (1-19725)

QY 1939 CTTCTTGGCGCCCTTCGCGGGCCATGTAGAGGAGCTGTACATGTTGACGGGTCCA 1880
Db 17234 ProSer---ArgProTyGlyArgProTrpAsnArgSerMetSerAsnTrpProGly--- 17251
QY 1879 TGTAGCCTGTAGTGGCGGCG-----GGATCGACGCGACGTCGGAAGCCCGCT 1832
Db 17252 -----AlaSerTrpArgSerSerArgTrpProGlyCys-----ArgThrSerProArg 17267
QY 1831 TCTGATCAGCT-----CGGGGTAGCGGGCTGAGGAGCGGAGC----- 1790
Db 17268 AlaGlyCysAlaTrpGlyArgTrpArgArgAlaGlySerGlyArgSerAlaArgCysSer 17287
QY 1789 -----GCAGATGACGATGCGCGCCGCAACCTGCTTGGCCAGGACCTCGGCA--- 1739
Db 17288 ThrProAlaArgThrGlyCys-----AlaSerSerAlaGlySerGlySerArgProPro 17305

QY 1738 ---GCTCGTTGG-----CCACGGGCATAT---CCAGCCAGTCCA--- 1706
Db 17306 ThrArgArgTrpProProProSerGlySerProArgLeuTyGlyThrAlaSerProTy 17325
QY 1705 -----CGTGGTCCATCAGAACCT---TGS-----TGTAGGTGC 1673
Db 17326 ThrSerThrTrpThrGlyProSerProGlyProProHisTrpSerSerArgCysThrCys 17345
QY 1672 CGCTTTGAGCTCTCCATGAAGAAGTTGGTGGAGACGGTCAGGTTGTCCACCCAGCCAC 1613
Db 17346 -----TrpTrpArgArgAla-----ProArgHis 17353
QY 1612 TCTTGGGTGGCAGAGCGG-----CCTCGCGCA 1583
Db 17354 AlaGlyProSerArgAlaGlyArgArgSerSerAlaArgCysTrpProArgArg 17373
QY 1582 GGTAGGTGGGCGAGTTGTGCGCGCAGGAACCTTGCCTGAGGACAGTTGTAGTAGA----- 1529
Db 17374 GlyArg-----ArgGlnAlaGlyCys-----AlaCysCysSerArgGlyGly 17387
QY 1528 -----AGT 1526
Db 17388 ProHisGlyAspGlyArgTrpArgProTrpArgArgSerAlaHisProSerArgProThr 17407
QY 1525 AGTTCTGCTTCGCGCAGTGCAGATTCTCCGCGCAGCCGTCATGGTGCAGCGATGTAGT 1466
Db 17408 ThrThrValCysHisArgCysSerProArgProArgSerThrCysCysAlaAlaArgAla 17427
QY 1465 TCTCAATGG-----GGATGCGCTCGCGCTTGATCAGCGCGTACTGCT 1424
Db 17428 ProArgTrpProProTrpSerThrSerSerCysAlaProPro-----SerThrThrAla 17445
QY 1423 TGCCCGCGCAGCCGCGCGCAACACACAGCAGCGCTTGTGTAAGAGCACCA----- 1373
Db 17446 CysSerProSerSerArg-----AlaAlaProProThrProArgArgProArgGlySer 17463
QY 1372 -----GGTCACGAACCTTGACGAACAGCAGCCACACCGG 1340
Db 17464 CysArgThrArgTrpProSerGlySerGlyProArgArgSerThrArgThrAlaGly 17483
QY 1339 GCTTGGGCGCGCTTCTCAGCAAGTGGATGACATGTTGCTGCCACAGACGGCGCTGCT 1280
Db 17484 SerHisCysAlaAlaThrArgProSer---AlaProAlaSerProSerProSerAlaGly 17502
QY 1279 CTTCCATTGTTGGGCGCGTGGCGAGCGCTTGAGCGTCTTCCCGCAGTCCAGCACCGG 1220
Db 17503 ArgSerSerAlaThrArgTrpGlySerAlaArgArgSerArgProSerProHisSerArg 17522
QY 1219 -----CCAGGC 1214
Db 17523 ThrProArgGlyArgAlaThrSerTrpTrpSerValArgProAlaCysSerThrGly 17542
QY 1213 ACTGACGACCCAGCACAGCTTGCCTGCGCCCTGGTAGTACAGGCGGTGCTGGAAGT 1154
Db 17543 ProGlyArgProArgSerAlaValCysCysAlaHisArgCysThrAlaProThrGlyArg 17562
QY 1153 ACCAGAGCGCTTGGCAGCAGAAAGTTGGTGGTTCGACAGGAAGCGCCAGCTTCT 1094
Db 17563 ThrArgSer-----ProThrGlyArgGlyGlyAlaAla 17573
QY 1093 TCTCGTACAGCTCTCAATGCGGGGTGACGCCCTGCGCGAAGAGCTGCC----- 1043
Db 17574 SerArgSerProProThrArgCysGlyAlaSerArgArgProGlyAlaAlaArgTrp 17593
QY 1042 -----ACAGTCTCTCAACT-----CCAGCTGCTGAATGGCA 1010
Db 17594 AlaCysSerSerTrpThrArgProThrThrArgileProGlyProAlaAlaProTrpPro 17613
QY 1009 CTTTCTTTCAGCTCCAGAAAGCGCCGACCTGCGGGGTTCAGTCCACCGACACACCTGGC 950
Db 17614 SerProSerGly-----ArgSerThrAlaThrAlaCysCysSerProValArgProTrp 17631
QY 949 CGGCCCCCTGCACCGCAGGTTTCAGGCGATTGACGCCCGCCCTAGTTCAGGGGTTCAGCACCG 890

```

Db 17632 ArgThrAlaSerArgSerSerAlaAlaTrpCys-----GlySerSerSer 17646
Qy 889 TGTCTTGGGGTTGATCTCCATACCTCCATATCGGGCTCGGGTCTCTCCACAGCTGCG 830
Db 17647 ProSerTrp-----ArgArgProSerThrSer--- 17655
Qy 829 TGTACAGGAAGTGGCGGGAACATGGCGCGCGCTCCACGGCTCTCTCGTGCAGGGCGT 770
Db 17656 ---ThrThrAlaTrp-----ArgAlaProArg----- 17663
Qy 769 GGCCAAACGCTGGCAGCGCGCAATCCACAGTAGTAGGGCGCG-----GCAGCC 719
Db 17664 -----ArgSerAlaArgArgSerHisArgSerIleCysAlaAla 17676
Qy 718 ACGCAGCTAGGGATCGAACCCCTGGGGTTCCTGCTCCACACGGCTCCAGCTTCGTGCT 659
Db 17677 ThrSerArgThrSerSerProAsnSerArgArgSerThrArgThrSerGlyArgSer 17696
Qy 658 CCAGGTAGCGCGCGCTCGGGCGCGATGTCATGTTGTCATGTCGAGATCGATCGCC 599
Db 17697 ProAlaArgArg-----Thr 17701
Qy 598 AGAAGAAACGGCGGACCCAGGGCATCTGGCGCAGGGCAGGTCTGTAATCTTCCGCTCAGCT 539
Db 17702 ArgArgProThrAlaArgProCysAlaProAlaThrSerTrpArg---CysAlaGlyArg 17720
Qy 538 AGAAGTGGCAACGCCACACAGGCGCTCTGGGACAGTACGACGACGCTGTCGATGA 479
Db 17721 ArgThrArgValArgSerGlyProArgArgCysThrGlyCysAlaArg----- 17736
Qy 478 CGTTGTGGAACGGTGGATCATCTGACGAGTAGGAGAGGTGATGAGCGTCCGGGTGC 419
Db 17736 ----- 17736
Qy 418 CCTCAGGGGGCAAAATGGCAAGCGTCTGGCTCCACGACCTGGACATTTCTCCAGCCCT 359
Db 17737 -----SerLeuArgArgProProArgThrGlyArgSer----- 17747
Qy 358 TGGCTTCTCGCTCTTCT-----TGGCCA-----CCTCGCACAGCG 323
Db 17748 TrpCysSerProArgSerGlyThrTrpGlnTrpTyrAlaArgArgSerArgThrArg 17767
Qy 322 AGTGGCAGCTCCACACAGT---AGATGGACTTCACTTCGCGAGGTTCGATGTAATCAG 266
Db 17768 ProGlyGlnGlyArgGlyAlaArgArgThrSerArgGlyProLysArg---GlyGlu 17786
Qy 265 CCATCATATCGACATTTCTCCCGAGTGCACCACCCAGGTCAACCCAGATGAGGTTTCGAGC 206
Db 17787 ProGlnArgMetArgGlyAlaArg---ArgTrpLysGlyGlnProArgArgThrArgArg 17805
Qy 205 GCTCG-----CCAGCGGGGCGAGAAAGCGAG-----CGG 176
Db 17806 AlaArgArgSerProProTrpGlyThrHisArgArgArgSerGlyArgGlyArg 17825
Qy 175 CTGGGGCCCTAGAGCTCTCCAGCGCAGCGGTGATCATCGCCCTCTTGTGTCGCA 116
Db 17826 AlaGlyCysArgAspArgGlyProGlyValCysSerGlyArgSerArgAlaAlaCysArg 17845
Qy 115 -----ACCACATATGGCGCAGAACCGTCAAGGTCACTCTTCATGTC 77
Db 17846 ProProAlaAspSerSerSerThrThrSerProProArgProValThrProTyrCys 17865
Qy 76 TGCTGAGCTTGAAGTCTCCAGGGAGAGTCTCTTGTGTGAGC----- 32
Db 17866 -----SerArgSerArgGlnAlaGluTrpAlaSerThrCysArgProPro 17881
Qy 31 -----TCGACAGCGCGCGCTCAGCACCGACCCGCCA 2
Db 17882 ProTrpSerSerAlaSerArgSerSerSerArgPro 17893

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RESULT 12

us-10-084-846A-4

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; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4

Alignment Scores:
Pred. No.: 3,07e-16 Length: 19725
Score: 407.00 Matches: 236
Percent Similarity: 34.8% Conservative: 48
Best Local Similarity: 29.0% Mismatches: 237
Query Match: 11.2% Indels: 294
DB: 4 Gaps: 53

US-10-620-914-44 (1-1947) x US-10-084-846A-4 (1-19725)
Qy 23 GGCCTGGGAGCTACACCAAGAAGAACTTCTCCCTGG-----AGAAGCTCAAGC 70
Db 17261 GlyCysArgThrSerProArgAlaGlyCysAlaTrpGlyArgTrpArgAlaGlySer 17280
Qy 71 TCAGCAGCATGAAGGATGACCTGACCGTTCTGCGGCATATGTGTTGGGACGACAGAGG 130
Db 17281 GlyArgSer-----AlaArgCysSerThrProAlaArg--- 17291
Qy 131 CGCATGATCAGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGGCCGCTGCTTTGCTG 190
Db 17292 -----ThrGlyCysAlaSerSerAlaGlySerGlySerArgPro--- 17304
Qy 191 CCCGCC-----TGGCCGAGCGCTCGAACCTCATCTGGGTTGACCTGGGTGGTGCAC 244
Db 17305 ProThrArgArgTrpProProProSerGlySerProArgLeu-----Tyr 17319
Qy 245 GGGAGAATGTCGATATGCTGATTCATCGACCTGGCGAAGTTCAAGTCCATCTAGC 304
Db 17320 GlyThrAlaSer-----ProTyrThrSerThrTrpGlyProSerProGlyPro 17336
Qy 305 -----TGCTCGACCTGTCGCTCGCTGCGAGGTGGCCCAAGAGA----- 346
Db 17337 ProHisTrpSer-----SerArgCysThrCysTrpTrpArgArgAlaProArgHis 17353
Qy 347 -----AGCGAAGG-----AGCGAAGG-----CCAAGGCT 364
Db 17354 AlaGlyProSerArgArgAlaGlyArgArgSerSerAlaArgCysTrpProArgArg 17373
Qy 365 GGAGA-----ATGTCAGGTCTG----- 382
Db 17374 GlyArgArgGlnAlaGlyCysAlaCysCysSerArgGlyGlyProHisGlyAspGlyArg 17393
Qy 383 TGGAGGCCGACGCTGCCAATTTGGCCCTCGCTGCGAGGTGGCCACCG-----CGAGCG 430
Db 17394 TrpArgProTrpArgArgSerAlaHisProSerArgProThrThrValCysHisArg 17413
Qy 431 TCATCACCTTCTCTACTCGCTACGATGATTCCACCGTTCCACACCGTCCACACGTCAC 490

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Db 17414 CysSerProArgPro-----ArgSerThrCysCysAlaAlaArg 17426
QY 491 CTTGCTCGTACCTGCCAAGACGGCTGGTGGGGCTTCCAGCTTCTACGTGACGGCA 550
Db 17427 AlaProArgTppProProTppSerThrSerSerCysAlaProProSerThrThraCys 17446
QY 551 AGTAGACACTGC-----CCCTGGCCGAGATGCCCTGGT 583
Db 17447 SerProSerSerArgAlaAlaProProThrProArgArgProArgGlySerCysArgThr 17466
QY 584 CGCGCGGTTCT---TCTGGCGATCGATCTCGACATCGACACATTCGACATCG----- 634
Db 17467 ArgTppProSerGlySerGlyProArgArgSerThrThrArgThrAlaGlySerHisCys 17486
QY 635 -----GCCCCGAGCGCGCGCTACCTCGGAGC 661
Db 17487 AlaAlaThrArgProSerAlaProAlaSerProSerProSerAlaGlyArgSerSerAla 17506
QY 662 AGAAGCTGG---AGCGGTGGGAGCAGA---ACACCCAGGGTTTCGATCCCTACGTGC 715
Db 17507 ThrArgTppGlySerAlaArgArgSerArgProSerProHisSerArgThrProPro--- 17525
QY 716 CGTGGCTGGCGCCCTACTACTAGTGTGGATGGCGGCTGCCAGCGTTGCCACGCC 775
Db 17526 ArgGlyArgAla----- 17529
QY 776 TGCACGAGGCGCGTGGAGCGCGCCCA---TGTTC---CGCCCACT 820
Db 17530 -----ThrSerTppSerValArgProAlaCysSerThrGlyProGlyArgProArg 17547
QY 821 TCC-----TGACAGCAGTCTGGGAGACCGCCAGCCGCGGATA 859
Db 17548 SerAlaValCysCysAlaHisArgCysThrAlaProThrGlyArgThrArgSerProThr 17567
QY 860 TGGAGGTATGG-----AGATCAACCCNAGGACACGGTCTGACCTGACTACGC 910
Db 17568 GlyArgGlyGlyAlaAlaSerArgSerProProSerThrArgCys-----Gly 17583
QY 911 CGCGTCAATGCCCTGAACCTGCTGGTGCAGGGGCGCGCCAGGTGGT-----CGG 964
Db 17584 AlaSerArgArgPro-----GlyAlaAlaArgTppAlaCysSerSer 17597
QY 965 TGGACTCAACCCCGCAGTGGCGCTTCTGGAGCTGAAGAAGTGGCCATTGACGACG 1024
Db 17598 TrpThr---ArgProThrThrArgileProGlyProAlaAlaProTppProSerProSer 17616
QY 1025 TGGAGTTGAGGACGTGGCAGCTGTTCCGGGAGGGCGTGCACCCGCGCATGGAGGC 1084
Db 17617 -----GlyArgSerThrAlaThrAlaCysCysSerProVal----- 17628
QY 1085 TGTACGAGAAGAGTGGCGCTTCTTGTGCAACACGACACCACTTCTGGTCCAAGC 1144
Db 17629 -----ArgProTppArgThrAlaSerArgSerSerAlaAlaTppCysGlySerSer 17645
QY 1145 GCC-----TCTGGTACTTCCAGCAGCGCC-----TGFACTACCGAGGCG 1183
Db 17646 SerProSerTppArgArgProSerThrSerThrAlaTppArgAlaProArgArgSer 17665
QY 1184 GCATGGGCAAGCTGTGGGTGCTGCAGTGCCTGGCGCTGGTGTGGAGTGGGCAGA 1243
Db 17666 AlaArgArgSerHisArgSerIleCysAlaAla-----ThrSerArg 17679
QY 1244 CGGTCAAGC-----GCCTCGCAGCGCCCAATGGAGGAGCAGCGCC--- 1288
Db 17680 ThrSerSerProAsnSerArgArgSerSerThrArgThrSerGlyArgSerProAlaArg 17699
QY 1289 -----GTCTGTGGGACAGCAACA-----TGCTCATCC 1315
Db 17700 ArgThrArgArgProThrAlaArgProCysAlaProAlaThrSerTppArgCysAlaGly 17719
QY 1316 -----ACTTCGTGAGAACGGGCCCAAGCGCTGGTGGTGTTCGTCAAGT----- 1363
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Db 17720 ArgArgThrArgValArgSerGlyProArgArgCysThrGlyCysAlaArgSerLeuArg 17739
QY 1364 -----TCGTGAGCCTGGTGC----- 1378
Db 17740 ArgProProArgThrGlyArgSerTppCysSerProArgSerGlyThrTppGlnTpp 17759
QY 1379 -----TCTTCAACAAGCGCGTGTGGTTCGGCGCGCGCTGCGCGGCAAGC 1426
Db 17760 TyrAlaArgArgSerArgThrArgProGlyGlnGlyArgGlyGlnAlaArgArgThrSer 17779
QY 1427 -----AGTAGCGCTCATCAAGCGCGCAGCGCAGCCATCCCA 1459
Db 17780 ArgGlyProLysArgGlyGluProGlnArgMetArgGlyAlaArgArgTppLysGln 17799
QY 1460 TTGAGAACTACATCGCGCGCA-----CCATGGACGGCGTGGCGGAGAACT 1504
Db 17800 ProArgThrArgArgAlaArgArgArgSerProProTppGlyThrHisArgArg 17819
QY 1505 CGCAG-----TGCCCAAGCAGA 1522
Db 17820 ArgSerGlyArgGlyArgAlaGlyCysArgAspArgGlyProGlyValCysSerGlyArg 17839
QY 1523 ACTACTTCTACTACAACTGCCTCACCGGCAAGTTCCTCGCGGACAACTGCCCCACTACC 1582
Db 17840 SerArgAlaAlaCysArgProProAlaAspSerSerSerThrThrSerProProArg 17859
QY 1583 -----TGGCGAGGCGCGCTTTCGCCACCTCAAGAGTGGCGTGGTGG--- 1624
Db 17860 ProValThrProTppCysSerArgArg-----SerArgGlnAlaGluTppAla 17875
QY 1625 ---ACAACCTGACGTCTCCACCAACTTCTTCATGGAGGAGCTCA----- 1666
Db 17876 SerThrCysArgProProProTppSerSerAlaSerArgSerSerSerArgProSerAsn 17895
QY 1667 ---AAGCGCGCACCTACACCAAGGTGATTCTGATGGACACCGTGGACTGGCTGG--- 1717
Db 17896 ThrArgArgSerProValPro-----ThrAlaTppAlaArg 17907
QY 1718 -----ATATGCCCTGGCCACAGAGCTGGCGGAGTGGCTGGGCA 1756
Db 17908 SerAlaArgSerAlaCysThrAlaCysSerAlaArgLysGlyTppThrAsnAlaTppCys 17927
QY 1757 AGCAGTTGGCGCGGGGCGCATCGTCATCTGGCGCTCGCTCCCTCAGCGCGCGCTAGC 1816
Db 17928 GlyCysTppArgThrSerProAlaCysSerThrLeuThrProAlaAlaAlaArg----- 17945
QY 1817 CCGAGCTGATCCAGAAGCGGGCTTCGACGTCGCTGCATCCGCGCGCCACTCAGGGCT 1876
Db 17946 ---SerProSerArgHisArg----- 17951
QY 1877 ACATGGACCGCTCAACATGTACAGCTCTTCTATACATGGCGCGCC 1921
Db 17952 -----ThrProSerThr---SerArgThrSerProTppProAla 17963
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RESULT 13

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US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLNENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
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; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PFI
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.:      8,56e-15      Length:      19695
Score:          383.50      Matches:      218
Percent Similarity: 34.2%      Conservative: 57
Best Local Similarity: 27.1%      Mismatches: 268
Query Match:      10.6%      Indels:      260
DB:               4         Gaps:        48

US-10-620-914-44 (1-1947) x US-10-084-846A-3 (1-19695)
QY 1945 AGTTGTCTCT---TCTTGGCGC-----CCTTCGGCGGGCCCATGTAGA 1907
DB 4930 SerCysValIleGlyTrpArgHisArgAlaLaProProAlaCysLeuProCysAla 4949
QY 1906 -----AGGAGCTGTACATATTGACGCGGTCCATGT-----AGCCCTGAGTGG 1865
DB 4950 CysCysArgCysCysAryCysTrpProArgProCysCysGlyThrAlaProArgAla 4969
QY 1864 CGCGCGGATCAGCGCAGTCGAGCCCGCTTCTGGATCAGCTCGCGGTAGGCGGGC 1805
DB 4970 Arg-----ThrTrpArgAspProAlaProGlyValProArgArg-----Gly 4984
QY 1804 TGAGGAGCGGAGCGGCAGATGACGATCGCCCGCGCGCAACCTGCTTGGCCAGGCACT 1745
DB 4985 MetArgArgMetSerArgArgGlyGlyCysCysSerProSerProTrpTrp----- 5001
QY 1744 CGGCAGCTCGTTGGCCACGCGGCATATCCAGCCAGTCCACGTGTCTCCATCAGAA- 1691
DB 5002 -----TrpPro-----SerArgGlyProAlaGluArgTrp 5011
QY 1690 -----TCACCTTGGTGTAGTGGCGGCTTTGAGCTCCTCCATGAGAAAGTTGTGGAGA 1637
DB 5012 SerAlaGlyThrTrpAlaSer-----HisAlaTrpTrpAla 5023
QY 1636 CGGTACAGTTGTCCACACGCGCACTCTTGAGGTTGGGAGGCGCCTCGCGCAGGTAGG 1577
DB 5024 ArgSer-----ProGlySer 5028
QY 1576 TGGGCGAGTTGTGCGCAGGAACTTTCGGGTGAGGAGGCGCCTCGCGCAGGTAGG 1523
DB 5029 PheSerAlaLeuArg-----CysSerAlaSerSerLeuPro 5040
QY 1522 TCTGCTTGGCAGGTGCGAGTTCTCCGCGCAGCGGTCCA----- 1484
DB 5041 GlySerThrTrpProSerSerProProSerThrProThrSerIleSerSerProArg 5060
QY 1483 -----TGGTGGCGGATGTCTCAATGGGATGCCGCTCGCTTGATCAGCGGT 1430
DB 5061 SerGlyTrpArgCysSerCysSerSerAlaTrpSerSerValThrProThrMetLysAla 5080
QY 1429 ACTGCTTCCCGCGCAGCGCGCGCCAGCACAGCAGCGCGCTTGTGAAGAGCACCGAGC 1370
DB 5081 ArgAlaAlaProGlyProProTrpGluSerSerAlaSerAlaCys---ArgSerProSer 5099
QY 1369 TCAGAACTTGACGAAACA---GCCACACAGCGGTGGGGCGGTTCTTCAAGAGTGGGA 1313
DB 5100 AlaValLeuTrpAspThrArgCysThrProAlaThrProArgThrAlaSerAlaSer--- 5118
QY 1312 TGACATGTTGCTGTCCACAGAGCGGCGTCTCT-----CCATTGTGGGCG 1265
DB 5119 -----CysArgSerProSerSerTrpAlaSerProAlaProProSerProCysTrpArg 5136
QY 1264 CGTTGGCAGGCGGTGTGACGGTCTTGGCCAGTCCCGACGACCGCCAGGCACTGCAGCA 1205
DB 1264 CGTTGGCAGGCGGTGTGACGGTCTTGGCCAGTCCCGACGACCGCCAGGCACTGCAGCA 1205

5137 GlyCysTrpAsnAlaGlyCysSerSerProGlyArgAlaProThrProSerTrpGlyPro 5156
1204 CCCAGCACAGCTTCCCGCATCGCGCCCTGTAGTACAGCGCGTGTGGAAGTACCAGAGC 1145
5157 ProProTrpLeuSerProAla-----GlyCysCysSerArgValSerSerProCysCys 5174
1144 GCTTGGACCAAGAGTGTGGCTGTGGTTCGACAGAGAGGCGCGCATCTTCTTCTCGTACA 1085
5175 AlaAlaValArgProTrpAlaCysCysAlaProSerArgSerProArgSerSerAla 5194
1084 GCTCTCAATCGCGGGTGTGACGCGCT----- 1058
5195 SerTrpTrpCysSerSerAlaProProCysAspAlaSerTrpSerGlyArgSerAlaGly 5214
1057 CGCGAAGAGCTGCCACAGCTCTCAAACTCCAGCTGCT-----GAATGGCCACCT 1007
5215 CysProThrAlaAlaCysSerHisSerProAlaSerCysCysProArgSerProPro 5234
1006 TCTTCAGCTCCAGAAGCGCGCACTGCGGGGTTCAGTCCACGACACCA----- 956
5235 SerSerAlaSerIleSerSerSerAlaProSerCysSerAlaProSerAlaArgArgPro 5254
955 -----CCTGCGCGCGCCCTGCACCA-----GCAGTTTCAGGGCATTTCAGC 914
5255 ArgArgProTrpArgTrpProAlaAlaAsnCysArgAsnSerSerProTrpTrpCysCys 5274
913 GCGCGCTAGTCA-----GGGTTCAGCA 893
5275 ArgArgSerSerProArgSerAlaArgProThrCysCysAsnSerAlaGlyAlaAlaAla 5294
892 CCGGTCTCTTGGGGTTCATCTCCATCATCTCCATCATCGGCTCGGGTCTCTCCACGACT 833
5295 ProCysGlyCysGly-----ProAlaSer 5302
832 GCGGTACAGAAGGTGGCGGGAACATGGCGCGCTCCACGCGCTCTCTCGTGCAGGG 773
5303 ProCysTrpTrpProSerSerAlaAsnTrpArgAlaAlaArgGlnArgArgCys--- 5321
772 CGTGGCCAAAGCTGGCGGCGGCAATCCACAGTAGTAGGGGCGCGCAGCAGCAGCA 713
5322 -----ArgTrpSerAla-----SerThrProCysAlaSerAlaCysSerThrAla 5336
712 -----CGTAGGGATCGAACCCCTGGGTGTCT 686
5337 AlaAspProAsnTrpSerSerProSerGlySerAsnSerAlaSerHisProArgCysSer 5356
685 ---GCTCCACACAGCGCTTCAGCTTCTGCTCCAGGTAGCGCGCGCTCGGGCGCGATGT 629
5357 ProCysTrpSerSerProCysAlaProProSerProArg-----ArgCys 5372
628 CAATGTTGT-----CGATGTGGAAGATCGATCGCCAGAGAAACGGCGCG 584
5373 SerThrCysSerThrAlaProArgArgAlaProArgProProValGlnLysArgValPro 5392
583 ACCAGGCGATCGCGCAGGCGGAGGTGCTGATCTGCGCTCAGCTAGAGTGGCAACGC 524
5393 SerPheAlaAspAsp---GlyAlaAlaAsnSerAlaArgGluMetProGluArgVal 5411
523 CCACAGCGCGCTCTGGGACA----- 503
5412 IleProSerArgIleProThrLysArgLeuSerSerLysGluCysArgSerValArgAla 5431
502 GGTACGAGCAGCTGCT-----CGATGACGTTGTGGAACGGTG 464
5432 GlySerSerLysProGluAsnArgGluValGlyTrpCysArgProThrCysThrSerVal 5451
463 GAATCATCTGTGAGCGAGTAGGAGGTGATGAGCGTTCGCGGTGCCCTCAGGGGGCGCAA 404
5452 LeuSerAlaSerSerTrpArgArgVal-----AlaSerAsnGlyProTrpAsnAla--- 5468
403 ATTTGGCAAGCGTCCGCGCTCCACAGCTGGAGATCTTCTCCAGCCCTTGGCCTTCGCTTCT 344
5469 ---AlaSerIleArgProLysArgProArgHisThrSerSerAlaGlySerProProAla 5487
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QY 343 TCT-----TGGCCA----- 335
Db 5488 ThrSerProLeuArgLysTrpProCysGlyArgArgSerArgArgGlyGlyAlaAsp 5507
QY 334 -----CCTCGCACAGGAGTGGCACA--- 314
Db 5508 ArgArgArgAsnSerIleCysCysMetArgAlaProGlyThrArgAlaArgThrAla 5527
QY 313 GGTCCACCACGCTAGA-----TGGCACTTGAAC-----TCGCCA----- 281
Db 5528 GlyArgProArgHisThrCysSerGlyThrTrpTrpAlaGlyThrCysSerProTrparg 5547
QY 280 -----GGTCGATGTAATCAGCCATCATCATCGACATCT 248
Db 5548 SerGlyArgAlaAlaThrAlaCysSerAlaArgTrpAsnSerProSer--AlaThrCysA 5567
QY 247 CCCAGTG-----CCACCACCCAGGTCAACCCAGATGAGTTGG 209
Db 5567 rgProfileArgThrAlaProAlaArgSerSerProProThrThrThrGluArgArg-Ser 5586
QY 208 AGCGTCGGCCAGCGCGG-----CAGCAAGGCGAGCGGCTGGG 170
Db 5587 ThrGly-----GlyGlyTrpAlaProAlaSerSerAlaAlaMetArgSerArgProgly 5604
QY 169 GCGCGTAGA-----AGCTCTCCAGGCGAGCGGTGATCATCGCCCTTCTTGGTCCGGA 116
Db 5605 AlaAlaSerGlyProAlaSerProGlySerAlaArg---TrpProProArgGlyCysArg 5623
QY 115 ACCCATATGGCGGAGACGGTCAGGTCTATCTTCATCTGCTGAGTGTGAGCTTCTCCA 56
Db 5624 ArgSer-----SerArgCysThrAlaValThrSerArgCysSerArgArgAlaSerPro 5641
QY 55 GGG 53
Db 5642 Gly 5642

RESULT 14
US-10-118-495-3
; Sequence 3, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-118-495-3

Alignment Scores:
Pred. NO.: 6.82e-15 Length: 416
Score: 379.50 Matches: 127
Percent Similarity: 43.1% Conservative: 68
Best Local Similarity: 28.1% Mismatches: 182
Query Match: 10.5% Indels: 75
DB: 4 Gaps: 20

US-10-620-914-44 (1-1947) x US-10-118-495-3 (1-416)

QY 691 ACCCAGGGTTCGATCCCTACGTGCGGGTGGCGGCCGCCCTACTAGTGTGATTGGC 750
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QY 790 GTGAGCGCGCCGCCCATGTTCCCGCCACCTTC-----CTGTACACGAGTCGTGG 840
Db 34 MetGluArg-----MetPheSerArgLeuPheHisGlyLeuValTrpProGlnIleTrp 51
QY 841 GAGGACCCCGAGCGCGATATGAGGTGATGAGATCAACCCCAAGGACACGCGTGTGCAC 900
Db 52 GluAspProAlaValAspMetAlaAlaLeuAlaIleArgProGlyAspArgLeuValAla 71
QY 901 CTGACTAGCGCGGCTGCAATGCCCTGAACTGTGTGTGAGGGGGCGCGCAGGTGGTG 960
Db 72 IleAlaSerGlyGlyCysAsnValLeuSerTrpLeuThrGlnGlyProGlySerIleLeu 91
QY 961 TCGGTGAGACTCAACCCCGCGCAGTCGGCGCTTCTGGAGCTGMAAGGTGCCATTCCAG 1020
Db 92 AlaValAspLeuSerProAlaHisValAlaLeuGlyArgLeuLysLeuAlaAlaArg 111
QY 1021 CAGCTG---GAGTTTGGAGCGTGTGGCAdTGTTCGGCGAGGGCGTGCACCCCGGCATT 1077
Db 112 ThrLeuProAspHisAlaAlaPhePheAspLeuPheGlyArgAlaAspLeuProglyAsn 131
QY 1078 GAGGAGCTGTACGAGAAGAGTGGCGCTTCTCTGTCTCGCAACACGACCACTTCTGG 1137
Db 132 AlaAlaLeuTrpArgHisIleAlaProAlaLeuAspGlyArgSerArgArgTrp 151
QY 1138 -----TCCAAAGGCTCTGGTACTTCCAGCAGCGCTGTACTTACCAG 1179
Db 152 GluAlaArgSerProPheGlyArgArgIleGlnLeuPheGluArgGlyPheTrpArgHis 171
QY 1180 GCGCGCATGGCAAGCTGTGTGTGTCTCAGTCCCTGGCGCTGTGTGTGGAGCTGGCG 1239
Db 172 GlyAlaLeuGlyArgPheIleGlyAlaAlaHisThrLeuAla-----ArgAlaAlaGly 189
QY 1240 AAGACCGTCAAGCGCTCGCAACCGCGCCCAATGAGAGGAGCAGCGCTGTGTGGAGAC 1299
Db 190 ThrAspLeuArgGlyPheLeuAspCysProAspIleGluAlaGlnArgSerPheTrp 209
QY 1300 AGCAACATGCTCATCCACTTCTGTGAAGAACGGCGCCCAAGCGCTGTGTGTGTCTGTC 1359
Db 210 AlaHisIle-----GlyPro-----LeuPheGlu 217
QY 1360 AAGTTCTGAGCTGTGTCTTCAACAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1419
Db 218 AlaProValValGlnAlaLeuAlaArgArgProAlaAlaLeuPheGlyLeuGlyIlePro 237
QY 1420 GCGAAGCAGTACGCGCTGATCAAGCGGAGCGC-----ATCCCATTTAGAGAAC 1467
Db 238 ProAlaGlnTrpAlaLeuLeuAlaGlyAspGlyAspValLeuProVal----- 255
QY 1468 TACATCGCGCACCATGAGCGGTGGCGGAGAACTCGCAC----- 1509
Db 256 -----LeuArgGlnArgLeuHisArgLeuLeuCysAspPhe 267
QY 1510 GTGCGCAAGCAGAACTACTTCTACTACAACCTGCTCACCGGCAAGTTCTCGCGCACAAC 1569
Db 268 ProLeuArgGluAsnTrpPheAlaPheGlnAlaIleAlaArgArgTrpProArgProgly 287
QY 1570 -----TGCCCCACTTACCTCGCGAGCGCGCTTTCGCCACCTCAAGAGTGGCGTG 1620
Db 288 GluGlyAlaLeuProProTrpLeuGluProThrAlaPheGluThrLeuArgGluAsn--- 306
QY 1621 GTGACACCTGACCGCTCTCCCAACTTCTTATGAGGAGGAGCTCAAGCGCGCACCTTAC 1680
Db 307 AlaGlyArgValGlnIleGluAsnArgSerLeuThrGluAlaLeuAlaAlaGluProGlu 326
QY 1681 ACCAAGTG-----ATTCTGATGACACCGCTGAGCTGGCTGATATCCCGTGGCC 1731
Db 327 GluSerIleHisGlyPheThrLeuLeuAspAlaGlnAspTrpMetThrAspAlaGlnLeu 346
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Db 347 ThrAlaLeuTrpArgGlnValThrArgThrAlaAlaProGlyAlaArgValIlePheArg 366
Qy 1792 -----TCCGCTCCCTCAGCCCGCCCTACCGGAGCTGATCCAGAGCGGGCTTC 1842
Db 367 ThrGlyAlaAlaAspLeuLeuPro-----GlyArgValProGluGluIleLeuGly 384
Qy 1843 GACGTGGCTCATCCCGCGCCCACTCAGGCG-----TACATGGACCGGTCAACATG 1896
Db 385 HisTrpArgAlaAspArgAlaAlaGlyGlnAlaGlyHisAlaAlaAspArgSerAlaIle 404
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Db 405 TyrGlyGlyPheHisLeuTyrArgArgAspAla 416

RESULT 15

US-10-620-914-3
; Sequence 3, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE OF INVENTION: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-620-914-3

Alignment Scores:
Pred. No.: 6.82e-15 Length: 416
Score: 379.50 Matches: 127
Percent Similarity: 43.1% Conservative: 68
Best Local Similarity: 28.1% Mismatches: 182
Query Match: 10.5% Indels: 75
DB: 4 Gaps: 20

US-10-620-914-44 (1-1947) x US-10-620-914-3 (1-416)

Qy 691 ACCCAGGTTCCGATCCCTAGTGCCTGGTGGCGCGCCCTACTACGTGTGGATTGGC 750
Db 2 ThrGlnPheAlaLeuThrHisLeuPro-----AlaProPro-----ValAla 15
Qy 751 GCGCTGCCACGGTTGGCCACCGCTTGAC-----GAGGAGCGC 789
Db 16 Arg-----GlnIleGlyAlaAlaValHisArgThrSerLeuLeuSerAlaGluGlyLeu 33
Qy 790 GTGAGCGCGCCCGCCATGTTCCCGCCACCTC-----CNCATACGACGTCGTGG 840
Db 34 MetGluArg-----MetPheSerArgLeuPheHisGlyLeuValTyrProGlnIleTrp 51
Qy 841 GAGGACCCCGGCGGATATGAGGTGATGGAGATCAACCCCAAGGACACCGTGTGACC 900
Db 52 GluAspProAlaValAspMetAlaAlaLeuAlaIleArgProGlyAspArgLeuValAla 71
Qy 901 CTGACTAGCGCGGTGCAATGCTGAACTGCTGTGTGAGGGCGCGCCAGTGTGTG 960
Db 72 IleAlaSerGlyGlyCysAsnValLeuSerTyrLeuThrGlnGlyProGlySerIleLeu 91
Qy 961 TCGGTGGACTCAACCCCGCCAGTCGCGCTTCTGGAGCTGAAGAGTGCCTATTCCAG 1020
Db 92 AlaValAspLeuSerProAlaHisValAlaLeuGlyArgLeuLysLeuAlaAlaArg 111
Qy 1021 CAGCTG---GAGTTTGGAGCGTGTGGCAGCTGTGTTCGGCGAGGCGGTGCACCCGCGCAT 1077

Search completed: May 5, 2006, 08:02:11
Job time : 441.5 secs

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Db 152 GluAlaArgSerProPheGlyArgArgIleGlnLeuPheGluArgGlyPheTyrArgHis 171
Qy 1180 GCGCGCATGGCAAGCTGTGCTGGTGTGCTGAGTCCCTGCGCGGTGGTGGAGTGGCG 1239
Db 172 GlyAlaLeuGlyArgPheIleGlyAlaAlaHisThrLeuAla-----ArgAlaAlaGly 189
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Db 190 ThrAspLeuArgGlyPheLeuAspCysProAspIleGluAlaGlnArgSerPhePheTyr 209
Qy 1300 AGCAACATGCTCATCCACTTCTCGTGAAGAACCGCGCCCAAGCGCTGTGGTGTGCTC 1359
Db 210 AlaHisIle-----GlyPro-----LeuPheGlu 217
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Db 218 AlaProValValGlnAlaLeuAlaArgArgProAlaAlaLeuPheGlyLeuGlyIlePro 237
Qy 1420 GCGAAGCAGTACGCGCTGATCAACGCGGCGCGC-----ATCCCATTTGAGAAC 1467
Db 238 ProAlaGlnTyrAlaLeuLeuAlaGlyAspGlyAspGlyAspValLeuProval----- 255
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Qy 1510 GTGCGCAAGCAGAACTACTTCTACTACATGCTCTACCGGCAAGTCTCTCGCGGACAA 1569
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Qy 1621 GTGACAACTACCGTCTCCACCAACTTCTCATGGAGGAGCTCAAAGCGCGCACCTAC 1680
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Qy 1681 ACCAAGGTG-----ATTCTGATGACCACTGGACTGCTGGATATGCCCGTGGCC 1731
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Qy 1732 AACGAGTGGCGGAGTGCCTGGCCAAAGCAGGTTCGCGCGCGCGCATCGTCTATCTGGCG 1791
Db 347 ThrAlaLeuTrpArgGlnValThrArgThrAlaAlaProGlyAlaArgValIlePheArg 366
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Db 367 ThrGlyGlyAlaAlaAspLeuLeuPro-----GlyArgValProGluGluIleLeuGly 384
Qy 1843 GACGTGGCTGCATCGCGCGCGCCACTCAGGCG-----TACATGGACCGGTCAACATG 1896
Db 385 HisTrpArgAlaAspArgAlaAlaGlyGlnAlaGlyHisAlaAlaAspArgSerAlaIle 404
Qy 1897 TACAGCTCTTCTACATGGCGCGCGGAAGGCGCC 1932
Db 405 TyrGlyGlyPheHisLeuTyrArgArgAspAla 416

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 5, 2006, 07:53:13 ; Search time 3.9 Seconds
(without alignments)
4621.353 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

Sequence: 1 atgggtcggtcgctgacgg.....gcgccaaagaaggacaactaa 1947

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 470810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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12: /SID55/ptodata/1/pubpaa/US60 NEW PUB.pepl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303.5	8.4	4440	9 US-10-194-487-525	Sequence 525, App
2	303.5	8.4	4440	9 US-10-195-883-525	Sequence 525, App
3	303.5	8.4	4440	9 US-10-195-888-525	Sequence 525, App
4	303.5	8.4	4440	9 US-10-195-889-525	Sequence 525, App
5	294.5	8.1	386	11 US-11-096-568A-21828	Sequence 21828, A

6	279.5	7.7	386	11 US-11-096-568A-21828	Sequence 21828, A
7	275	7.6	1886	9 US-10-515-868-8	Sequence 8, Appli
c	270	7.5	495	11 US-11-182-016-31	Sequence 31, Appl
9	267.5	7.4	428	11 US-11-096-568A-19503	Sequence 19503, A
10	267.5	7.4	493	11 US-11-096-568A-11657	Sequence 11657, A
11	267.5	7.4	544	11 US-11-096-568A-19501	Sequence 19501, A
12	267	7.4	1076	9 US-10-131-826A-219	Sequence 219, App
13	267	7.4	1076	9 US-10-973-115B-219	Sequence 219, App
14	267	7.4	1076	9 US-10-137-873A-219	Sequence 219, App
15	267	7.4	1076	9 US-10-152-370-219	Sequence 219, App
16	267	7.4	1076	11 US-11-290-153-219	Sequence 219, App
17	264.5	7.3	1141	11 US-11-217-995-35	Sequence 35, Appl
18	263.5	7.3	1894	9 US-10-194-487-37	Sequence 97, Appl
19	263.5	7.3	1894	9 US-10-195-883-97	Sequence 97, Appl
20	263.5	7.3	1894	9 US-10-195-888-97	Sequence 97, Appl
21	263.5	7.3	1894	9 US-10-195-889-97	Sequence 97, Appl
22	262.5	7.3	1141	11 US-11-217-995-36	Sequence 36, Appl
23	262.5	7.3	1742	11 US-11-182-016-23	Sequence 23, Appl
24	262	7.2	413	11 US-11-096-568A-20771	Sequence 20771, A
25	261	7.2	1356	9 US-10-894-592-3	Sequence 3, Appli
26	258.5	7.1	766	11 US-11-096-568A-19864	Sequence 19864, A
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28	256	7.1	1652	11 US-11-241-631-1	Sequence 1, Appli
29	255	7.0	375	11 US-11-096-568A-21618	Sequence 21618, A
c	254.5	7.0	459	11 US-11-096-568A-21887	Sequence 21887, A
31	253	7.0	2508	11 US-11-241-631-7	Sequence 7, Appli
32	253	7.0	2544	11 US-11-241-631-3	Sequence 3, Appli
33	253	7.0	2601	11 US-11-241-631-9	Sequence 9, Appli
34	251.5	6.9	1128	11 US-11-241-631-11	Sequence 11, Appl
35	250.5	6.9	758	11 US-11-096-568A-14593	Sequence 14593, A
c	249.5	6.9	493	11 US-11-096-568A-11657	Sequence 11657, A
c	248.5	6.9	413	11 US-11-096-568A-20771	Sequence 20771, A
c	247	6.8	428	11 US-11-096-568A-19503	Sequence 19503, A
c	246.5	6.8	544	11 US-11-096-568A-19501	Sequence 5, Appli
40	246.5	6.8	1917	11 US-11-241-631-5	Sequence 5, Appli
41	245	6.8	639	9 US-10-915-002-247	Sequence 247, App
42	244.5	6.8	1743	9 US-10-194-487-451	Sequence 451, App
43	244.5	6.8	1743	9 US-10-195-883-451	Sequence 451, App
44	244.5	6.8	1743	9 US-10-195-888-451	Sequence 451, App
45	244.5	6.8	1743	9 US-10-195-889-451	Sequence 451, App

ALIGNMENTS

RESULT 1

US-10-194-487-525
; Sequence 525, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C132
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-525

Alignment Scores:
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Score: 303.50 Matches: 130
Percent Similarity: 36.3% Conservative: 52
Best Local Similarity: 25.9% Mismatches: 212
Query Match: 8.4% Indels: 108
DB: 9 Gaps: 17

US-10-620-914-44 (1-1947) x US-10-194-487-525 (1-4440)
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QY 527 TTGCGCGCTTACGTGAGCGGCAAGTACGACCTGCGCCCTCGCGC----- 571
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QY 626 TTGACATCGGCGCGCGCGCTTACCTGTGAGCAGAGCTGGAGCGCGTGTGGGAGC 685
Db CysThrThrAlaThrAlaCysAlaThrThrThrThrThrThrAlaAlaThrAlaCys----- 3869
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QY 1088 ACGAGAAGAAGCTGGCGCCCTTCTGTGCAAAACCCAGCCCAACTTCTGTGTCACAGCGCC 1147
Db Thr-----AlaThrCysCysCysAlaCysAlaThrThrGly-----Ala 3995
QY 1148 TCTGTACTTCCAGACGCGCTGTACTACGAGGCGCATGGGCAAGCTGTGTGGTGC 1207
Db GlyAlaThrCysAlaThrAlaCysThrGlyAlaAlaThrAlaThrAlaCysAlaGlyAla 4015
QY 1208 TGCAGTGCCTGGCGGTGTGCTGGGACTGGGCAAGACCGTCACGCGCTCGCCAAACGCGC 1267
Db CysThrAlaAlaThrThrCysAlaGlyAlaAlaAlaAlaAlaAlaAlaThrGlyThr--- 4034
QY 1268 CCACAATGGAGGAGCAGCGCGCTGTGTGGCAGCAACATGCTCATCCACTTCTGTGAAGA 1327
Db -----AlaThrGlyThrCysThrThrThrAla----- 4043
QY 1328 ACGGGCCCAAGCCGCTGTGTGCTGCTGCTCAAGTTCGTGAGCCTGGTGTCT- 1381
Db -----ThrThrGlyCysAlaThrThrGlyAlaGlyThrCysThrCys 4058
QY 1382 TCAACAAGCGCTGTGTGCTGCGCGCGCGCTGCGGCGGCAAGCAGTACGCGTGTATCA 1441
Db ThrThrAlaThrCysCysAlaAlaThrAlaAlaAlaAlaAlaAlaGlyAla----- 4075
QY 1442 AGCGGACGCGCATCCCATTTGAGAACTACATCGCGCGCACCATGGACGCGGTGGCGGAGA 1501
Db -----ThrAlaThrGlyAlaAlaThrThr----- 4084
QY 1502 ACTGCGACGTGCGCAAGCAGAACTACTTCTACTACACTGCTCACCGCAAGTTCCTGTC 1561
Db -----CysCysAlaThrGlyThrAlaThrThrGlyAlaAlaAlaThrCysThrCys 4102
QY 1562 GCGNACACTGCGCCACCTACTGCGCGGCGCGCTTGCACCCCTCAAGAGTGGCGTGG 1621
Db AlaCysThrGlyAlaGlyAlaCysThrThrAlaThrThrThrThrThrGlyGlyCysThr 4122
QY 1622 TGAACAACCTGACCGCTCCACCAACTTCTTCTGAGAGAGCTCAAAAGCGCGCACTACA 1681
Db ThrThrThr---CysAlaCysAlaThrGlyThrCysCysThrGlyCysAlaAlaAlaThr 4141
QY 1682 CCAAGGTGATTCGATGGACACGCTGCTGGCTGGATATGCT-----CCGTGGCGCA 1732
Db -----GlyThrAlaThrThrGlyThrThrAlaAlaAlaThrThrAla 4156
QY 1733 ACGAGCTGGCGGAGTGCCTGCGCAAGCAGGTGCGCGCGGCGCATCGTATCTGGCGCT 1792
Db ThrThrThrThrThrAlaGlyGlyThrAlaThrThrThrThrThrThrThrThrThrGlyAla 4176
QY 1793 CCGCTCCCTCAGCCCGCCCTAGCGCGAGCTGATCCAGAAGCGGCGCTTCGACGCTGGCT 1852
Db AlaAlaThrGlyAlaThrThr-----ThrCysThr 4187
QY 1853 GCATCCCGCGCGCACTCAGGGCTACATGACCGCGTCAACATGTACAGTCTCTTCTACA 1912
Db AlaAlaAlaGlyThrThrThrGlyThrAlaThrThrThrThrThrThrThrThrThrThrThr 4207

RESULT 2
US-10-195-883-525
; Sequence 525, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

QY	473	ACAA	CGT	ATC	GAC	GCAG	CGCT	TGCT	CGT	TAC	CTG	TCC	CAAG	CG	-----	GCT	TGT	GG	CG	CG	526	
Db	3794	Thr	Thr	Thr	Gly	Ala	Gly	Cys	Thr	Ala	Thr	Cys	Thr	Thr	Thr	Thr	Thr	Gly	Ala	Thr	3813	
QY	527	TTG	CCG	ACT	TCT	ACG	TG	GAG	GCG	CAAG	TAC	GAC	CTG	CGCC	TGCG	CG	-----				571	
Db	3814	Cys	Thr	Thr	Thr	Thr	Cys	Ala	Ala	Ala	Cys	Cys	Ala	Cys	Ala	Cys	Thr	Gly	Cys	Thr	3833	
QY	572	-----	AG	TG	CC	TG	TG	CG	CG	CG	TTT	CTT	CT	GCG	AT	CG	AT	CTT	CG	AC	625	
Db	3834	Thr	Thr	Ala	Cys	Thr	Gly	Ala	Ala	Cys	Thr	Gly	-----	Thr	Cys	Ala	Thr	Cys	Ala	Thr	3851	
QY	626	TTG	AC	AT	CG	CC	CG	CG	CG	CG	CG	CTT	AC	CTG	GAG	CAG	AG	AG	CTG	GAG	685	
Db	3852	Cys	Thr	Thr	Ala	Thr	Ala	Cys	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Ala	Thr	Ala	Cys	-----	3869
QY	686	AGA	AC	CCC	AGG	GT	T	CG	AT	CC	CT	TAC	GT	G	CG	TG	CG	CG	CG	CG	-----	730
Db	3870	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	730	
QY	731	---	CC	T	A	C	T	A	C	T	G	T	G	G	C	G	C	T	G	C	CG	787
Db	3882	Gly	Thr	Thr	Thr	Cys	Thr	Cys	Ala	Ala	Thr	Gly	Cys	Cys	Ala	Cys	Thr	Cys	Thr	Thr	3901	
QY	788	GCG	TG	GAG	CG	CG	CG	CG	CG	CG	CG	AT	G	T	T	C	C	G	T	C	847	
Db	3902	Thr	Thr	Cys	Ala	Gly	Ala	Gly	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Cys	Thr	Gly	Gly	Thr	3921	
QY	848	CCG	AG	CCG	G	A	T	A	T	G	G	A	G	T	G	A	T	G	A	T	907	
Db	3922	Thr	Gly	Thr	Ala	Ala	Gly	Ala	Thr	Gly	Thr	Thr	Thr	Ala	Thr	Cys	-----	Thr	Thr	Cys	3941	
QY	908	GCG	CG	CG	T	G	C	A	T	G	C	C	T	G	A	A	C	T	G	T	967	
Db	3941	hr	Gly	Gly	Ala	Thr	Ala	Ala	-----	Ala	Cys	Thr	Thr	Thr	Ala	Gly	Ala	Ala	Thr	Cys	3960	
QY	968	ACT	G	C	A	A	C	C	C	G	C	G	C	G	T	T	C	T	G	A	1027	
Db	3961	Thr	Cys	Thr	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	3963		
QY	1028	AGT	T	T	G	A	G	A	C	G	T	G	T	T	C	G	G	C	G	G	1087	
Db	3964	---	Thr	Thr	Thr	Gly	Thr	Cys	Cys	Ala	Ala	Gly	Thr	Ala	Ala	Ala	Ala	Thr	Ala	3982		
QY	1088	AC	G	A	G	A	A	G	A	G	C	T	T	C	T	G	T	C	G	T	1147	
Db	3983	Thr	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	3995		
QY	1148	TCT	GG	T	A	C	T	T	C	C	A	C	G	C	G	T	C	T	A	C	1207	


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Pred. No.: 3,78e-11 Length: 4440
Score: 303.50 Matches: 130
Percent Similarity: 36.3% Conservative: 52
Best Local Similarity: 25.9% Mismatches: 212
Query Match: 8.4% Indels: 108
DB: 9 Gaps: 17

US-10-620-914-44 (1-1947) x US-10-195-889-525 (1-4440)
QY 473 ACAAGCTCATCCAGCAGCGCTTCTGCTGCTCCCAAGAGC-----GCCGTGGGGC 526
Db ThrThrThrGlyAlaGlyCysThrAlaThrThrThrThrThrThrGlyAlaThrThrCys 3813
QY 527 TTGCGCATCTTACGTGAGCGGCAAGTAGCAGCTGCCCTGGGCC----- 571
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 3814
QY 572 -----AGATGCCCTGTCGCGCGCTTCTTCTGGCGATCGATCTTCGACATCGACA 625
Db ThrThrAlaCysThrGlyAlaAlaCysThrGly-----ThrCysAlaThrCysAlaThr 3851
QY 626 TTGACATCGCGCCGAGCGCGCTACCTGGAGCAGAAGCTGGAGCGGTGGGAGC 685
Db ThrThrThrAlaThrAlaCysAlaThrThrThrThrThrThrThrThrThrThrThrThr 3852
QY 686 AGAACACCCAGGTTCCATCCCTAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
Db ThrCysAlaGlyCysAlaAlaGlyAlaCysAlaAla 3881
QY 731 ---CCTACTAGTGTGGATTGGCCCGCTGCCAGCGTTGGCCACCGCTTCGACGAGG 787
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 3882
QY 788 GGTGGAGCGCGCCCATGTTCCCGCCACCTCTCTGTACACGCGAGTGGGGAGGACC 847
Db ThrThrCysAlaGlyAlaGlyThrThrThrThrThrThrThrThrThrThrThrThrThr 3902
QY 848 CCGAGCGGATATGAGGTGATGAGATCAACCCCAAGACACAGGTGTGACCTTGACTA 907
Db ThrGlyThrAlaAlaGlyAlaThrThrThrThrThrThrThrThrThrThrThrThrThr 3922
QY 908 GCGGCGGTGCAATCCCTGACCTGCTGGTGCAGGCGCGCGCGCGCGCGCGCGCGCG 967
Db ThrGlyThrAlaAlaGlyAlaThrThrThrThrThrThrThrThrThrThrThrThrThr 3941
QY 968 ACTGCAACCCCGCGCAGTCCGGCTTCTGGAGCTGAAGAAGTGGCCATTGACGAGCTG 1027
Db ThrCysThr----- 3963
QY 1028 AGTTTGGAGACGTGTGGAGCTGTTTCGGCGAGGGCGTGCACCCGCGCATTTGAGGAG 1087
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 3964
QY 1088 ACGAGAAGNAGCTGGCGCCCTTCTCTGTCGCAACCCAGCCACCACTTCTGTTCCAGCG 1147
Db Thr-----AlaThrCysCysCysAlaCysAlaThrThrGly-----Ala 3995
QY 1148 TCTGTACTTCCAGCAGCGCTGTACTACAGGGCGCATGGCAAGCTGTGCTGGGTGC 1207
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 3996
QY 1208 TGCAGTGTGCGCTGGTGTGGAGCTGGGCAAGCCGTCAAGCGCTCCAGCGCTCCCAAGCG 1267
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 4016
QY 1268 CCACAATGGAGGAGCGCGCTGTGGGACAGCAATGCTCATCCACTTCGTGTGAAGA 1327
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 4035
QY 1328 ACGGGCCCAAGCGCTGGTGTGGCTGTTCTGCTCAAGTTCGTGAGCCTGGTGTCT----- 1381
Db ThrGlyCysAlaThrThrGlyAlaGlyThrCysThrThrCys 4044
QY 1636 CGG-----TCAGTTGTTCACCGCCACTCTTTGAGGGTGGGGAAGGCCCGCTCGCGCA 1583
```

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QY 1382 TCAACAGGCCGCTGCTGTGGTTCGGCGCGCGCGCGCGCAAGCAGTACGGCTGATCA 1441
Db ThrThrAlaThrCysCysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 4059
QY 1442 AGGCGGAGCGCATCCCATTCAGAACTACATCGCGCGCACCATGACGGCTGGCGGAGA 1501
Db ThrAlaThrGlyAlaAlaThrThrThr----- 4084
QY 1502 ACTCGCAGCTCGCAAGCAACTACTTCTACTACACTGCTCACCAGCAAGTTCTCTGC 1561
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 4085
QY 1562 GCGCAACTGCGCCACCTACCTGCGGAGGGCGCTTCCGCCACCTCAAGAGTGGCGTGG 1621
Db AlaCysThrGlyAlaGlyAlaCysThrThrAlaThrThrThrThrThrThrThrThrThr 4103
QY 1622 TGGCAACTCAGCTGCCCACTCCCACTTCTCATGGAGAGCTCAAGCGCGCACTACA 1681
Db ThrThrThr-----CysAlaCysAlaThrGlyThrCysCysThrGlyCysAlaAlaAla 4141
QY 1682 CCAAGTGATTCGATGGACCCAGCTGGACTGGCTGGATATGC-----CCGTGGCCA 1732
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 4142
QY 1733 ACGAGTGGCGGAGTGGCTGCCCAAGCAGGTGGCGCGCGCGCATCGTATCTGGCGCT 1792
Db ThrThrThrThrThrAlaGlyThrAlaThrThrThrThrThrThrThrThrThrThrThr 4157
QY 1793 CGCGCTCCCTCAGCGCGCTACCGCGAGCTGATCCAGAAGCGGGCTTCGACGTCGCT 1852
Db ThrAlaThrGlyAlaThrThrThr-----ThrCysThr 4177
QY 1853 GCATCCGCGCGCCACTCAGGGCTACATGGACCGCTCAACATGTACAGCTCTCTTCTACA 1912
Db ThrAlaAlaGlyThrThrThrThrGlyThrAlaThrThrThrThrThrThrThrThrThr 4188
RESULT 5
US-11-096-568A-21828
; Sequence 21828, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
; FILE OF INVENTION: Thebby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21828
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(386)
; OTHER INFORMATION: Ceres Seq. ID no. 12406424
US-11-096-568A-21828
Alignment Scores:
Pred. No.: 1,02e-10 Length: 386
Score: 294.50 Matches: 127
Percent Similarity: 37.4% Conservative: 26
Best Local Similarity: 31.1% Mismatches: 117
Query Match: 8.1% Indels: 139
DB: 11 Gaps: 28
US-10-620-914-44 (1-1947) x US-11-096-568A-21828 (1-386)
QY 1684 TGGTGTAGTGGCGCGCTTTCAGCTCTCCATCAAGAAAGTTGGTGG-----AGA 1637
Db ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 35
QY 1636 CGG-----TCAGTTGTTCACCGCCACTCTTTGAGGGTGGGGAAGGCCCGCTCGCGCA 1583
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Db	55	ArgProGlyProGlyArgAlaProArgGlyAlaAlaGlyProArgArgPro-----	71
Qy	1582	GGTAGGTGGGCGACGTTGCGC-----	1562
Db	72	---GlyGlyGlySerThrArgArgLeuLeuAlaLeuAlaArgGlnProGlnMetProArg	90
Qy	1561	---GCAGGAACCTCCCGGTGAGGCGAGTTGTAGTAGAAAGTAGTTCTGCTGCGCACGTCGC	1505
Db	91	GlySerGlyAlaSerArgProGlySerCysSer-----SerArgGly	104
Qy	1504	AGTTCTCCGCCACCGCTCATGTCGCGCGATGTAGTTCTCAATGGGATGCCGTCGC	1445
Db	105	SerThrProArgArg---TrpProAla---AlaGlyGlyArgTrp-----	118
Qy	1444	CCTTGATCAGCGCGTACTGCTTGCCCGGCA-----CGCCGCCCGGAACC	1400
Db	119	-----ArgThrProCysProCysAlaSerProSerProArgArgAlaArgPro	134
Qy	1399	ACAGCAGCGCCTTTGTAAGAGACACACAGGCTCACAACTTGACGAACAGACACACACAGCG	1340
Db	135	ThrAlaAlaGlyGlyAlaThrSerThrGlyCys-----SerThrAlaThrAlaAla	151
Qy	1339	---GCTTGGGCGCTTCTTCACGAAGTGGATGAGCATGTTGCTGTCCACAGACGGCGCT	1283
Db	152	ArgThrTrpProArgArgAlaGlyThrGlyCysThrThrCysSerPro-----	167
Qy	1282	GCTCTCCATTGTGGGCGCTTGCGAGGCGCTTGACGGCTTGCCAGTCCCGACGACCA	1223
Db	168	-----ArgSerSerProLeuProSerPro-----	175
Qy	1222	-----CGCGCAGGC-----ACTGCAGCACCCAGCAGACGCTTGC	1190
Db	176	ProThrAlaProArgArgProGlyProProArgTrpAsnAlaAlaSerArgGlyTrpThr	195
Qy	1189	CCA-----TGCCGCCCTGTGTAGTACAGGCGGTGCGAAGTACCAGA-----	1148
Db	196	ProArgCysArgProAlaGlyAlaProProAlaAlaAlaThrArgThrSerAlaThr	215
Qy	1147	-----GGCGCTTGGACCAAGAGTTGTGCTGGTTGCGACA	1112
Db	216	ThrTrpAlaProProProTrpTrpProSerTrpArgSerAlaAlaSerTrpTrpProThr	235
Qy	1111	GGAAGGCGCCAGCTTCTTCGTACAGCTCCTCAATGC-----GGGGGTGCACGCGCT	1058
Db	236	-----ValAlaThrAlaAlaArgCysAlaAlaGlyAlaAlaArg	249
Qy	1057	CGCGAAGACAGTGCACACGTCCTCAAACTCCAGCTGCT-----GAATGG-----	1013
Db	250	ArgArgCysArgCysArgArgThrThrSerProThrAlaProThrSerTrpSerGlySer	269
Qy	1012	---CCAGCTTCTCAGTCCAGAACGCCGACTCGCGGGGTTCAGTCCACCGACACCA	956
Db	270	ArgProArgAlaAlaAlaSerSerGlyArgAlaArgAlaCysTrpAlaSerSerPro	289
Qy	955	CCTGGCGCGCCCTGCACACAGAGTTTCAGGCAATTGCACGCGCCGCTAGTCAGGGTCA	896
Db	290	-----CysProAlaProSerGlyThrAlaThrSerSerArgThr-----Ser	303
Qy	895	GCAACGTTCTTGGGGTTGATCTCCATCACTCCATATCCG-----GTCGGGGTCT	842
Db	304	ArgProCysProArgSerArgSerProThrAlaProThrProThrSerAlaSerSerSer	323
Qy	841	CCACAGACTGGGTACAGNAGTGGGGGAACATGGGGCGCGCTCCACCGGCTCT	782
Db	324	ProAlaThrAla-----SerGlyThrTrpLeuAlaThr-----ArgPro	336
Qy	781	CGTGCAGGCGTGGCCAAACGCTGGGCGAGCGCCAAATCCACAGTAGTAGGGGCGCGCA	722
Db	337	ArgAla-----ArgTrp-----Arg	341
Qy	721	GCCACGCACGTAGGGGATCGAACCCCTGG-----TGTTCTGCT	683

Db 342 AlaProAlaSerAlaGlyGlyProGlyGlyAlaProArgProProArgCysSerPro 361
 Qy 682 CCCACAGCGCTCCAGCTTCTGCTCCA 656
 Db 362 SerTrpProSerProGlyAlaAlaPro 370

RESULT 6
 US-11-096-568A-21828
 ; Sequence 21828, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Pol
 ; TITLE OF INVENTION: Theby
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096.568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 21828
 ; LENGTH: 386
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(386)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12406424
 US-11-096-568A-21828

Alignment Scores:
 Pred. No.: 8,46e-10 Length: 386
 Score: 279.50 Matches: 126
 Percent Similarity: 36.4% Conservative: 31
 Best Local Similarity: 29.2% Mismatches: 123
 Query Match: 7.7% Indels: 151
 DB: 11 Gaps: 22

US-10-620-914-44 (1-1947) x US-11-096-568A-21828 (1-386)

Qy 711 CGTCCGTGGCTGCGCGCCCTACTACGTGTGGATTGCGCGCTCCCGAGCTTGGCCA 770
 Db 37 ArgCysAlaAlaThrArgTrpProGlnArgHisArgTrpProAspArgArgArgPro 56
 Qy 771 CGCCCTGCACGAGAGCGCGTGGAGCGGCCCCCATGTTCCCGCCCACTCTCTCTGTACAC 830
 Db 57 GlyProGlyArgAlaProArgGlyAlaAla----- 66
 Qy 831 GCAGTCGTGGAGAGACCCCGAGCCGGATATGAGGTGATGAGATCAACCCCAAGGACAC 890
 Db 67 -----GlyProArgArgProGlyGlySerThr----- 76
 Qy 891 GGTGCTGACCTGACTAGCGCGCGCTG-----CAATGCCCTGAA 929
 Db 77 -----ArgArgLeuLeuAlaAlaArgGlnProGlnMetProArg 90
 Qy 930 CCTGCTGTGTGACGGGGCGCCAGGTGTGTTCGGTGGACTGTCACCCCGCGACGTGCGC 989
 Db 91 GlySerGlyAla--SerArgProGlySerCysSer-----SerArgGly 104
 Qy 990 GCTTCTGGAGCTGAAGAAGTGGCCATTCACAGCTGGAGTTTGAGGACGTGTGCGACGT 104
 Db 105 SerThrGlyPro--ArgArgTrpProAlaAlaGlyGlyArgTrpArgThrProCysPro 124
 Qy 1050 GTTCGGCGAGGGCGTGCACCCGCGCATTTAGGAGCTGTACGAGAAGAAGCTGGCGCCCTT 110
 Db 124 ySAlaSer-----ProS 128
 Qy 1110 CCTGTCGCAACACGACCCACAACTTCTGTGTCCAGGCGCTCTGGTACTTCCAGCAGCGCT 116
 Db 128 erProArgArgAlaArgProThr-----AlaAlaGlyGlyAlaThrSerThrGlyC 145
 Qy 1170 GTACTACGAGGGCGCA-----TGGGCAAGCTGTGTGGGTGC---TGCAGTGCCT 121
 Db 145 ySserThrAlaThrAlaAlaArgThrTrpProArgAlaGlyThrGlyCysThrThr- 164

Db 1247 ----- 1247
QY 1277 AGGACACGGCGTGTGGGACAGACACATCTCATCTCCACTTGTGTGAAGAACGGGCCCA 1336
Db 1248 ---AlaAlaAlaThrCys---AlaAlaThrCysAlaThrThrAlaAlaAlaGlyGlyAla 1265
QY 1337 AGCGCTGGTGGCTGTTCGTCAGTTCGTGAGCC----- 1372
Db 1266 AlaThrCysCysAlaCysAlaAlaAlaGlyCysAlaAlaAlaCysAlaGlyAlaGlyThr 1285
QY 1373 TGGTCTCTTCAACAGCCCGTGTGTGTTCGCGCGCGGTGCGCGGCAAGCAGTACG 1432
Db 1286 ThrCysAlaGlyThrCysThrCysAlaThrThrGlyCysAlaAlaGlyGlyThr 1305
QY 1433 CGTGTCAAGCGGACGGCATCCCATTTGAGAACTACATCG----- 1474
Db 1306 ---AlaAlaAlaThrAlaThrCysAlaThrThrThrAlaAlaThrThrGlyGlyAla 1323
QY 1475 ---CGCGCACCATGACGCGGTGGCGGAGAACTCGCAGTGTGGCAAGCAGAACTACT 1528
Db 1324 AlaGlyThrAlaGlyThrThrAlaAlaAlaThrGlyThrCysThrCysAlaThrThr 1343
QY 1529 TCTACTACAACTGGCTACCGGCAAGTTCCTGCGGCAACAACTGCCCACTACCTGCGCG 1588
Db 1344 GlyThrThrThrAlaThrThrGlyAlaCysAla-----CysAla 1357
QY 1589 AGGCGGCTTCGCCACCCCTCAAGAGTGGCGGTGGAGCAACTGACCGTCTCCACCAACT 1648
Db 1358 ThrCysThrAlaThrAlaThrAlaThrAlaCysAlaThrThr----- 1371
QY 1649 TCTTCATGAGGAGCTCAAGCGGCACCTACACCAAGGTGATCTGTGATGACACCACTGG 1708
Db 1372 -----ThrGlyThr-GI 1375
QY 1709 ACTGCTGTGATATGCCGTGGCCAAACGAGCTGGCGAGTGTGCTGGCCAAAGAGTGTGCG 1768
Db 1375 yAlaAlaGlyCysAlaAlaGlyAlaAlaAlaCysAlaAlaThrAlaAlaAlaAlaAl 1395
QY 1769 CGGGGGCATCGTATCTGGCGCTCCGCTCCCTCAGCCCGCCCTACGCCGAGTGATCC 1828
Db 1395 agly---CysThrThrCysGlyThrAlaThrGlyCysAlaThrThr----- 1410
QY 1829 AGAAGGCGGCTGCGACTGCGTGCATCCGCGCGCCACTCAGGGCTACATGACCGCG 1888
Db 1411 -----AlaAlaThrThrAlaAlaCysAlaAlaAlaAlaThrAlaThrGlyThrAla 1428
QY 1889 TCACATGT-----ACAGTCTCTTCT 1909
Db 1429 ThrThrCysAlaGlyThrAlaCysThrGlyAlaThrThrGlyCysAlaThrAlaCysAla 1448
QY 1910 ACATGGCCCGCGGAGGGCGCCAGAGGACAACCT 1945
Db 1449 AlaGlyAlaThrGlyCysAlaThrGlyThrThrThr 1460

RESULT 8

US-11-182-016-31
; Sequence 31, Application US/11182016
; Publication No. US2006001929A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-31
Alignment Scores: 3.32e-09 Length: 495
Pred. No.: 270.00 Matches: 150
Score: 270.00
Percent Similarity: 30.7% Conservative: 40
Best Local Similarity: 24.3% Mismatches: 171
Query Match: 7.5% Indels: 257
DB: 11 Gaps: 34
US-10-620-914-44 (1-1947) x US-11-182-016-31 (1-495)
QY 1811 GCGCGGCTGAGGAGCGGAGCGCCAGATGACGATGCGCCGCGGCAACCTGCTTG--- 1755
Db 2 GlyGlyCysArg-----LysAspValTrpLusSerProGlyHisCysCysIleTrp 18
QY 1754 -----GCCAGGCACTCGCCAGCTCGTTGGCCACGCGC----- 1722
Db 19 GlyAspArgLeuSerLeuProSerArgGluProGlyLeuIleLeuThrGlyGlyPro 38
QY 1721 -----ATATCCAGCCAGTCCAGTGGTCCATCAGATCACGATCACCTTG 1683
Db 39 IleProGlyArgValLeuAsnValAsnSerGlnAla----- 50
QY 1682 GTGTAGGTGCGCGCTTTGAGCTCTCCATGAAGAAGTTGGTGGAGACGGTCAGGTGTGCC 1623
Db 51 -----SerSerSerSerAsnLysGluAlaMetSerGluArgGlyArg 64
QY 1622 ACCACGCCACTCTTGGAGTGGCGAAGCGCGCTCGCGCAGGTAGTGGGCGAGTGTGCG 1563
Db 65 AlaArgCysAlaLeuSerLeuThrGlnAla-ProArgSer-----Trp----- 78
QY 1562 CGCAGGAACCTTCCGCGTGGAGCAGTGTGTAGTAAGTAGTCTCTGCGCAGCTGCGAG 1503
Db 79 -GlnGlyThrCysGlnAsnGlyHisProAlaHisSerHisAlaThrSerLeuArgArgSe 98
QY 1502 TTCTCCCGCAGCGCTCCATGGTGGCGCGATGTAGTTCTCAATGGGATGCCGTCGCC 1443
Db 98 f-----ProArg----- 100
QY 1442 TTGATAGCGGTACTCTTTCGCGGACGCGCGC-----CGCCGAACCCAGCAGCAGGCC 1389
Db 101 -----CysProGlySerArgGlyGlnArgArgSerLeu----- 111
QY 1388 TTGTTGAAGACACAGGCTCAGCAACTTGAAGACAGCCACACAGCGGCTTGGGCGCG 1329
Db 112 -CysArgArgLeuProGlySerArgThrGlyHisGlyHisArgAlaLeuAlaHisAlaPr 131
QY 1328 TTCTTCAGGAAGTGCATGTCGTGTGCCACAGCGCGCTGCTCTCCATCTG 1269
Db 131 oGlyProGluCysGlyGlnCysAlaGlnSerGlnHisLeuAlaAlaProValGI 151
QY 1268 GCGCGCTTGGCGAGCGCTTGACGGTCT----- 1241
Db 151 yAlaAlaArgArg-----ArgSerProAlaLeuGluValProHisThrGlnProPr 168
QY 1240 -----TGCCAGTCCAGCAGCAGCG----- 1220
Db 168 oLeuLeuProAlaProAspMetGluGluCysTrpAlaProAlaProGlnGlnGlyAspLe 188
QY 1219 -CCAGGCACCTGACAGCAGCAGCTTGGCCATGCGCCCTGGTAGT---ACAGGCGCG 1164
Db 188 uProTrpAlaLeuArgTrpGlnGlnLeuAlaLeuCysGlnSerGlySerLeuValGlyAl 208
QY 1163 TGCTGGAAGTACAGAGCGCT-----TG 1140
Db 208 aAlaSerAlaGlyArgGlySerSerAlaCysGlnAlaGluAspTrpArgTrpArgTrpTr 228
QY 1139 GACCAAGAGTGTGGCTGG-----TTTGGACAGGAAGGCGCGCAGCTTCTTCGTACAG 1083
Db 228 pThr-----TrpProSerProSerAlaLysSerProSerGlyAlaArgGlnTh 244

```

QY 1082 TCCT-----CAATGCGCGG 1068
Db 244 rProAlaHispeGlySerLeuLyProLeuLeuAlaAlaProThrSerCysSerG1 264
QY 1067 TGCAGCCCTCGCCGACAGCTGCCACACGCTCTCAACTCCAGCTGCTGAATGCCAC 1008
Db 264 yGlyTrpProArgHisProAla-----ProAspSerAlaAlaProGlyValGlnPr 281
QY 1007 T-----TCTTCAGCTCCAGAGCCGCGACTCGCGGGGTTGCACTCCACCCGACAC 954
Db 281 oHisAlaAlaHisAlaProGlyAlaProAlaProAlaAlaValProProArgProAl 301
QY 953 TGGCCGCGCCCTGCA----- 938
Db 301 aAlaPheProProAlaAspGlySerProProSerLeuLeuTrpProArgSerCysLe 321
QY 937 -----CCAGCAGGTTTC 927
Db 321 uTrpGlnProPheSerGlnThrArgHisTrpSerSerGlyThrGlnSerProLeuGlyPr 341
QY 926 AGGCATTGCAGCCCGCTAGTCAGGGTTCAGCACCGTGT----- 887
Db 341 oGly---ValProArgProGlySerGlyHisSerProCysGluSerCysSerTrpHisLe 360
QY 886 ---CCTTGGGTTGATCT-----CCATCACTCCATATCCGGTCCGG-- 848
Db 360 uLySerProTrpProSerProCysThrGlnAlaProHisProProArgProValArgTr 380
QY 847 ---GGTCTCCACGACTCGGTGTACAGGAAGTGGCGGGAACATGGCGGCGCG 795
Db 380 pSerHisGlyProProSerGlySerTrpPro-----TrpCysArgGlyTrpHisArgLe 398
QY 794 TCCACGCGCT-----CCTCGTCGAGGGGTGGCCAAAGCTGGCGAGCGGCCA 747
Db 398 uProSerAlaHisArgSerArgProArgLeuSerSerGlyGlnIleTrpAla----- 415
QY 746 ATCCACAGTATAGGGGGCGGACGCCAGCAGTATAGGGATGAACCTCGGTGTTC 687
Db 416 ---ValGlnSerTrpGly---ProSerLeuCysArgArgArgThrSerProSerArgCy 433
QY 686 TGCTCCACACGCGCTCAGCTTCTGCTCCAGTAGGCGCGCGCTCGGGCCGATGTC 627
Db 433 sAlaProProSerProProGlyHisProProLeuCysGlnProArgGly---CysHi 452
QY 626 ATGTTGTCGATGTCGAGATCGATCGCCAGAGAAGAACCGCGCACCGGCATCTCG 567
Db 452 sCysCys----- 454
QY 566 AGGGCAGGTGCTATTCGCCCTCAGTAGAGTCCGCAACGCCACCGCGCTCTTGG 507
Db 455 -----CysLeuHisArgArgGluProSerArg----- 463
QY 506 GACAGGTACGACGAGCTGCTCGATGACGTGTGGAACGGTGGNAATCATCGTAGCGAG 447
Db 464 -SerGlyThrSerArgPro----- 469
QY 446 TAGGAGAAGGTGATGAGCGTCCGCTGCGCTCAGGGGGCGCAAAATGGCAAGCGTCG 387
Db 470 -----ProAlaAlaArgArgPr 474
QY 386 T-----CCACGACCTGGACATCTTCCAGCCCTTGGCTTCGCT 347
Db 474 oLeuAlaAlaLeuAlaArgSerGlySerGlySerProProTrpProAlaPro 491

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RESULT 9

```

US-11-096-568A-19503
; Sequence 19503, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thetby
; FILE REFERENCE: 2750-1592PUS

```

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; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19503
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(428)
; OTHER INFORMATION: Ceres Seq. ID no. 12373378
US-11-096-568A-19503

Alignment Scores:
Pred. NO.: 4,65e-09 Length: 428
Score: 267.50 Matches: 126
Percent Similarity: 41.6% Conservative: 30
Best Local Similarity: 33.6% Mismatches: 103
Query Match: 7.4% Indels: 116
DB: 11 Gaps: 30

US-10-620-914-44 (1-1947) x US-11-096-568A-19503 (1-428)

QY 205 CGCTCGAACCTCATCTGGTTGACCTGGTGGT---GCACCTGGGGAGAAATGTCGATATG 261
Db 131 ArgGlyAsnIleLeuSerTyrAsnLeuGlyGlyHisGly-LeuGlnArg----- 146
QY 262 ATGGCTGATTATACATCGACCTGGCGAAGTTCAAAGTCCATCTACGTGG---TCGACCTGTGC 318
Db 147 -----ArgAlaSerSerProSerIleTrpProAlaThrCysSe 159
QY 319 CACTCGCTGTGCGAGGTGGCCAGAAAGACGAAAGGCGTGGAGAAATGTCGAC 378
Db 159 r-----ArgProAlaAla-----Ar 164
QY 379 GTCGTGAGGCGCAGCTTGCACATTTGCCATTTGGCCCTCGAGGCGACCGACCTCATCACC 438
Db 164 gAlaTrp---ProTrpTrpSerAlaArgPro-----SerProSerArgGlyThrPr 181
QY 439 T-----TCTCTACTCGCTCACGATdTATCCCGTTCCACACGTCATCGACCAG 489
Db 181 oGlySerGlyAlaProCysSerSerArg-----ThrProSerSerGlyPr 196
QY 490 GCTTGTCTGATCTGCT-----CCCAAGACGCG 516
Db 196 oAlaAlaArgArgCysCysProThrGlyAlaAlaThrSerThrAlaProSerThrSe 216
QY 517 CTGG-----TGGCGTTGCGGACTTCTACGTGAGCGGCAAGTAGCAGCTGCCCTGCGC 570
Db 216 rTrpSerThrTrpCysAlaArgThr-----ArgAlaArgThrThrAlaProSerAl 233
QY 571 CAGATGCCCTGGTGGCGCGTTTCTTCTGCGATCGATCTTCGACATCGACATCGACAATTGAC 630
Db 233 aProCysThrArgArgArgThrSerSerGlySerArg----- 245
QY 631 ATCGGCCCCGAGCGCCCGCTACCTCGAGCAGAAAGTGGAGCGGTGTGGAGCAGAAC 690
Db 246 -AlaCysProSerAlaAlaThrCysTrp-----ArgTrpAlaAlaThrArgSerArgPr 263
QY 691 ACCCAGGGTTCGA---TCCCTCAGTGGCTGGCTGGCGGCCCTACTACGTGGATT 747
Db 263 oThrSerProArgTrpGlyProTrpCys-----CysProSerProSerCysSerSe 281
QY 748 GGCC---GCCTGCCAGCGTTTGGCCACGCTGACGAGGAGCGGTGGAGCGCGCGCC 804
Db 281 rSerArgAlaCys-----Cys-----SerAlaThrCysSerArgPr 293
QY 805 ATGTTCCCGCCCACTTCTCTGTACACGCACTGCTGGGAGGACCCCGAGCGGATATGAG 864
Db 293 o-----ArgProPro-----ArgArgArgArgProGlnGlyThrProAr 308
QY 865 GTGATGAGATCAACCCCAAGGACACCGGTGCTGACCTGACTAGCGGCGGTGCAATGCC 924
Db 924 -----

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Db 308 gProProArgProThrSerArgThr-----SerSerAlaAlaArgSe 321
Qy 925 CTGAACCTGCTGGTCAGCGGGCGCGCCAGGTGGTGTGCTGGAAGTCAACCCCGCGCAG 984
Db 321 rSerThrSerAlaCysThrArgProAlaAlaThrCys----- 333
Qy 985 TCGGCGCTTCGGAGCTGAAGAAGTGGCCATTGACAGCTGGAGTTTGAGGAGC----- 1039
Db 334 -----TrpSerThrCysArg-----AlaThrTrpAlaCysAlaThrProTh 347
Qy 1040 -----TGTGGCAGCTGTTCGGCGAGGCGGTGCACCGCGCATTTGAGGAGCTG 1086
Db 347 rTIpArgProProAlaProArgCysThrAlaSerAlaThrProGlnAlaAlaSerGl 367
Qy 1087 TACAGAGA---AGAGAGTGGGCCCT---TCTGTGCGMAACGACGACCAACTTCTGTGTC 1140
Db 367 yThrSerTrpArgThrTrpArgProArgAlaAlaSerAlaAlaThrAlaSerGlySe 387
Qy 1141 AAGCGCCTCTGTACTTCCAGCAGCGGCTGTACTACCAAG-----GCGGCATGGCAAG 1194
Db 387 rSerProSerGlyArgAlaSerAlaAla---ThrAlaArgCysGlyAlaProSerAlaAl 406
Qy 1195 CTGTGCTGGTGTCTGCAGTGCCTGCGCGCTGG---TGCTGGGAC 1234
Db 406 aCysAlaAlaProArgAlaAlaProGlyTrpAspCysValAsp 420

RESULT 10
US-11-096-568A-11657
; Sequence 11657, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11657
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(493)
; OTHER INFORMATION: Ceres Seq. ID no. 15219800
US-11-096-568A-11657

Alignment Scores:
Pred. No.: 4,72e-09 Length: 493
Score: 267.50 Matches: 154
Percent Similarity: 31.7% Conservative: 38
Best Local Similarity: 25.4% Mismatches: 127
Query Match: 7.4% Indels: 287
DB: 11 Gaps: 29

US-10-620-914-44 (1-1947) x US-11-096-568A-11657 (1-493)
Qy 161 TCTACGGGCCCCAGGCGCGCTGCTTTGTGTCGCGCGCTGGCGGAGCTCGAACCTCATCT 220
Db 31 SerAlaSerProProProProProProProProProProArgAlaTrp----- 43
Qy 221 GGGTTGACCTGGTGGGCACTGGGGAGATGTCGATATGATGCTGATTACATCGACC 280
Db 44 -----AlaSerThr 46
Qy 281 TGGCGAAGTTCAAGTCCATCTACGTGGTCG-----ACCTGTGGCACTCGC 325
Db 47 Trp---AlaSerSerProSerThrArgThrAlaGlyAlaLeuProThrCysArgAlaArg 65
Qy 326 TGTGCGAGGTGCCCAAGAGGCGAGGCGCAAGGCTGGAAGAATGTCAGGTCTGGTGG 385
Db 66 ArgArgCysTrpAlaGlyProSerArgArgPro----- 76
```

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Qy 386 AGCCCGACGCTTGCCAAATTTGGCGCCCTTGAGGSCACCGCGACGCTCATCACCTTCTCCT 445
Db 77 -----ArgSerProSerArgProSerProAlaPro 86
Qy 446 ACTCGCTCAAGATGATTCCACCGTTCCACAACGTCATCGACCAAGCTTGCTCGTACCTGT 505
Db 86 ----- 86
Qy 506 CCCAAGACGGCTGTGTGGGCGTTGCCAGCTTCTACGTGAGGGCAAGTACGACCTGCCCC 565
Db 87 -----ThrSerTrpAlaAlaSerProThr----- 94
Qy 566 TGCGCCAGATGCCCTGTGTCGCGCGTTTCTTCTGGCGATCGATCTTCGACATCGACAACA 625
Db 95 -----GlyArgAla---ThrArgAlaThrArgAlaThrAlaThrThr 108
Qy 626 TTGACATCGGCGCGGCGCGCTTACCTGGAGCAGAAAGCTGGAGCGGTGTGGGAGC 685
Db 109 -----AlaArgPro----- 111
Qy 686 AGAACACCCAGGTTTCGATCCCTTACGTCCGTGGTGGCGGCCCTTACTACTGTGTGGA 745
Db 112 -----ProPro----- 113
Qy 746 TTGGCGCCTGCCAGCGTTGGCCACGCTGCACGAGGAGCGGTGGAGCGCGGCCCA 805
Db 114 -----ProAlaThrArgSerSerThrSerProArgPro 124
Qy 806 TGTTCGCGC-----CCACCTTCTGTACACGC---AGTCGTGGGAGGACCCCGAGCGG 856
Db 125 ThrThrArgSerProProProProProProProProProProProProProProProSerArg 144
Qy 857 ATATGAGGTGATGAGATCAACCCCAAGACAGCGGTGCTGACCTGACTAGCGCGCGCT 916
Db 145 -----ArgProSerThrArg----- 149
Qy 917 GCAATGCCCTGAACCTCTGTGTGAGGCGCGCGCGAGGTGGTGTGCTGGTGGACTGCAAC 976
Db 150 -----AlaSerGlyProSer----- 154
Qy 977 CCGCGCAGTCGGCGCTTCTGGAGCTGAAGAAGTGGCCATTACAGCAGCTGGAGTTTGAG 1036
Db 155 -----GlyAlaSer 157
Qy 1037 ACGTGTGGCAGCTGTTCGGCGAGGCGGTGCACCCGCGCATTGAGGAGCTGTACAGAGA 1096
Db 158 ThrSerGlyProSerSerProSerAla-----AlaThrArgArg 170
Qy 1097 AGCTGGCGCCTTCTGTGCAAAACCAAGCCACAACCTTCTGTGTCGAAGCGCTCTGTGTA 1156
Db 171 Ser---ArgProSerAlaAlaArgPro---ArgArgSerAlaProAlaAlaSerAlaThr 188
Qy 1157 TCCAGCACGGCGCTGT-----ACTACAGGCGCGCATGGGCAAGCTGTGTGGTGTGTC 1210
Db 189 ThrArgThrThrAlaProThrThrArgAlaSerAlaAla----- 202
Qy 1211 AGTCCTGGCGGTGGTGTGGTGGTGGAGCTGGGCAAGACCGTCAAGCGCTCGCCACGCGCCA 1270
Db 203 -----ThrSerArgThrProProSerPro 210
Qy 1271 CAATGGAGGAGCAGCGCGTCTGTGGGACAGACAATGCTCATCTCATCTTCGTGAAGAAGC 1330
Db 211 Arg-----SerThrSerSerProThr 217
Qy 1331 GGCCCAAGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1390
Db 218 GlyProSer-----SerArgSerProSerProThrSerProSerSer 232
Qy 1391 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1450
Db 233 ProSerProSerProThrSerProArgThrCysSerSerAlaAlaProSerThrArgThr 252
```

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QY 1451 GCATCCCGATTGAGAACTACATCGCGCGCACCATGAGCGCGCTGGCGGAGAACTCGCAGC 1510
Db 253 ThrAlaPro-----ThrThrAlaSerThrPro-----ArgArgProAlaAlaSer 267
QY 1511 TCGCGAAGCAGAACTACTTCTACTCAACTGCTCACCGGCAAGTTCTCTGGCGGCAAACT 1570
Db 268 SerAlaSerArgThrAlaSerSerSerArgSerProProProThrThrProSerSerAla 287
QY 1571 GCCCAACCTACCTGCGCGAGCGGCTTCGCCACCTCTCAAGAGTGGCGTGGTGGACAACC 1630
Db 288 AlaSerPro-----ArgArgThrArgProProSer----- 297
QY 1631 TCACCGTCTCCACCAACTCTTCATGGAGGAGCTCAAGCGCGCACTACACCAAGGTGA 1690
Db 298 -----SerProProThr----- 301
QY 1691 TTCTGATGACCACTGGACTGGCTGGATATGCCCGTGGCCAAACGAGCTGGCGGAGTGCC 1750
Db 302 -----ProSerSer 304
QY 1751 TGGCCAAAGAGTTGCGCGGCGGCATCGTCATCTGGCGCTCCGCTCCCTCAGCCCGC 1810
Db 305 ProProSerCysAlaArgProAlaAlaSerSerProGlyThrLeuSerCysSerAlaSer 324
QY 1811 CCTACCGCGAGCTGATCC-----AGAAGCGGGCTTCGACGTGCGCTGCATCCGCC 1861
Db 325 AlaThrSerSerSerThrSerAlaAlaProSerSerIleCysLeuSerThr 344
QY 1862 GCGCCACTCAGGGCTACATGAGCGCGCTCAACATGTACAGCTCCCTTCTACATGGCGCGCC 1921
Db 345 ArgLeuArgArgSerSerLeuArgThrArgMetThrSer----- 358
QY 1922 GGAAGGGCGCCAAAGG 1939
Db 359 -----IleProArgArg 362
```

RESULT 11

```
US-11-096-568A-19501
; Sequence 19501, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19501
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 12373376
US-11-096-568A-19501
```

Alignment Scores:

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Pred. No.: 4, 77e-09 Length: 544
Score: 267.50 Matches: 126
Percent Similarity: 41.6% Conservative: 30
Best Local Similarity: 33.6% Mismatches: 103
Query Match: 7.4% Indels: 116
DB: 11 Gaps: 30

US-10-620-914-44 (1-1947) x US-11-096-568A-19501 (1-544)
QY 205 CGCTCGAACCTCATCTGGTGTGACCTGGTGGT---GGCATGGGGAGAAATGTCGATATG 261
Db 247 ArgGlyAsnIleLeuSerTyAsnLeuGlyGlyHisGly-LeuGlnArg----- 262
QY 262 ATGGCTGATTTACATCGACCTGGCGAAGTTCAAGTCCATCTACGTGG---TCGACCTGTGC 318
```

RESULT 12

US-10-131-826A-219

```
Db 263 -----ArgAlaSerSerProSerIleThrProAlaThrCysSe 275
QY 319 CACTCGCTGTGCGAGTGGCCAAAGAGGCGCAAGGGCTGGAAGAATGTCAG 378
Db 275 r-----ArgProAlaAla-----Ar 280
QY 379 GTCTGGAGGCGCAGCTTGGCAATTTTCGCCCTGAGGGCACCGCAGCTCATACC 438
Db 280 gAlaIrp---ProTrpTrpSerAlaArgPro-----SerProSerArgGlyThrPr 297
QY 439 T-----TCTCTACTCTCCTCAGATGATTCACCGTTCACCAAGCTCATCCACAG 489
Db 297 oGlySerGlyAlaProCysSerSerArg-----ThrProSerSerGlyPr 312
QY 490 GCTTGTCTGCTCTGT-----CCCAAGCAGCGC 516
Db 312 oAlaAlaArgArgCysCysProThrGlyAlaAlaThrSerThrAlaProSerThrSe 332
QY 517 CTGG-----TGGCGGTTCGCACTTTCACGTAGCGGCAAGTACGACCTGCCCTCGCC 570
Db 332 rTrpSerThrTrpCysAlaArgThr-----ArgAlaArgThrThrAlaProSerAl 349
QY 571 CAGATGCCCTGCTGCGCGCTTCTTCTGCGCATCGATCTTCGACATCGACAACATTGAC 630
Db 349 aProCysThrArgArgThrSerSerGlySerArg----- 361
QY 631 ATCGCCCGCGCGCTTCTGAGCAGAGCTGGAGCGCGCTGGGAGCAGAAC 690
Db 362 -AlaCysProSerAlaAlaThrCysTrp-----ArgTrpAlaAlaThrArgSerArgPr 379
QY 691 ACCCAGGGTTCGA---TCCCTACGTGCGCGTGGCTGCGCGCCCTCTACTAGTGTGGATT 747
Db 379 oThrSerProArgTrpGlyProTrpCys-----CysProSerProSerSerCysSe 397
QY 748 GGCC---GCCTGCGCGAGTGGCCCGCTGACGAGGAGCGCGCTGGAGCGCGCCGCC 804
Db 397 rSerArgAlaCys-----Cys-----SerAlaThrCysSerArgPr 409
QY 805 ATGTTCCCGCCACCTTCTGTACACGCAAGTGGCGGAGGACCCCGAGCCGATATGAG 864
Db 409 o-----ArgProPro-----ArgArgArgArgProProGlnGlyThrProAr 424
QY 865 GTGATGAGATCAACCCCAAGCAGCGTGTGACCTGACTAGCGCGCTGCAATGCC 924
Db 424 gProProArgProThrSerArgThr-----SerSerAlaArgSe 437
QY 925 CTGAACCTGTGCTGCGAGGGCGCGCGCAGGTGTGTGCTGGTGGACTGCAACCCCGCGCAG 984
Db 437 rSerThrSerAlaCysThrArgProAlaAlaThrCys----- 449
QY 985 TCGCGCTTCTGAGCTTGAAGAGGTGGCCATTCAGCAGCTGGAGTTTGAGGAGC----- 1039
Db 450 -----TrpSerThrCysArg-----AlaThrTrpAlaCysAlaThrProTh 463
QY 1040 -----TGTGCGAGCTTTCGGGAGGCGCTGACCGCGCTGACCGCGCTGAGAGCTG 1086
Db 463 rTrpArgProProAlaProArgCysThrAlaSerAlaThrProGlnAlaAlaSerGl 483
QY 1087 TAGCAGA---AGAAGCTGGCGCCT---TCTGTGCGCAACCGACCACTTCTGTGTC 1140
Db 483 yThrSerTrpArgThrTrpArgProArgAlaAlaSerAlaAlaThrAlaSerGlySe 503
QY 1141 AAGCGCTCTGGTACTTCCAGCAGCGCTGTACTACCAGG-----GGCGCATGGGCAAG 1194
Db 503 rSerProSerGlyArgAlaSerSerAla---ThrAlaArgCysGlyAlaProSerAlaAl 522
QY 1195 CTGTGCTGGTGTGTCAGTGCCTGGCGCTG---TGCTGGGAC 1234
Db 522 aCysAlaAlaProArgAlaAlaProGlyTrpAspCysValAsp 536
```



```
QY 1655 TGGAGGAGCTCAAGCGCGCACCTTACACCAAGGTGATTCTGATGGACCACTGGACTGGC 1714
Db 576 -----
QY 1715 TGGATATGCCGTGGCCCAACGAGCTGGCGAGTGCCTGGCCCAAGCAGGTGGCGCGGCG 1774
Db 577 -----CysAlaGlyThrThrAlaThrThrThrThrGlyAlaAlaAlaThrAlaCysAla 594
QY 1775 GCATCGTCATCTGGCGCT-----CGCCCTCCCTCAGCCGCGC 1810
Db 595 AlathrAlaAlaGlyAlaAlaCysThrGlyCysThrAlaGlyAlaAlaAlaThrAlaThr 614
QY 1811 CCTAGCGGAGTGTACAGAGGCGGCTTCGAGCTGCGTGCATCGCGCGCCACTC 1870
Db 615 GlyThrThrAlaThrAlaAlaCysAlaGlyThrCysThrAlaThrThrThrCysThr 634
QY 1871 AGGCTACATGACCGCTCAACATGTACAGCTCCTCTTACA 1912
Db 635 ThrThrThrAlaAlaAlaAlaCysThrThrThrThrThr 648

RESULT 13
US-10-973-115B-219
; Sequence 219, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-219

Alignment Scores:
Pred. No.: 5,53e-09 Length: 1076
Score: 267.00 Matches: 121
Percent Similarity: 33.7% Conservative: 52
```

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Best Local Similarity: 23.5% Mismatches: 223
Query Match: 7.4% Indels: 118
DB: 9 Gaps: 17
US-10-620-914-44 (1-1947) x US-10-973-115B-219 (1-1076)
QY 482 TCGACACAGGCTTGTCTGTCTACTGTCCCAADACGCGCTGGTGGCGGTGGCCGACTTCTACG 541
Db 216 AlathrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 235
QY 542 TGAGCGCAAGTACGACCTGCCCTGGCCAGATGCCCTGTGTGGCGCGCTTCTTCTTCTGGC 601
Db 236 Alalalalalalalalalalalalalalalalalalalalalalalalalalalalalalal 254
QY 602 GATCGATCTTCGACATCAACAATTGACATTCGCCGCCGAGCGCGCGCTTACCTGGAGC 661
Db 255 -----CysAlaGlyThrThrAlaThrThrAlaThrGlyAlaAlaAlaAlaAlaCysThr- 270
QY 662 AGAGCTGGAGCGGTGTGGAGGAGCAGAACACCCAGGGTTGATCCCTACGTGCGGTGGC 721
Db 271 -----GlyThrCysAlaAlaAlaThrThrCysAlaAlaGlyAlaAlaCysAlaGly 287
QY 722 TGGCGCGCC-----CCTACTACGTGTGATTGGCGCGCTGCCCGCGGTG 766
Db 288 CysThrThrCysThrGlyThrCysCysCysThrThrCysThrThrCysAlaAlaThrGlyGlyAla 307
QY 767 GCCACGCGCTGCACAGAGGCGGTGGAGCGCGCGCCCATGTTCCCGCCACCTTCTCTGT 826
Db 308 AlaglyAlaCysGlyThrThrThrThrThrGlyGlyThrCysAlaAlaCysThrGlyCys 327
QY 827 ACAGCAGTGTGGAGGAGCCCGAGCGCGGATATGGAGGTGATGAGATCAACCCCAAGG 886
Db 328 AlaAlaThrThrGlyCysAlaAlaGlyGlyCys----- 338
QY 887 ACAGGTGTGACCCCTGACTAGCGCGCTGCAATGCCCTGAACCTGTGTGTGAGG--- 943
Db 339 ThrGlyCys-----AlaAlaGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 355
QY 944 -----GGCGCGCGAGGTGTGTGTGGAGCTGCAACCCCGCGCAGTGGCGC 991
Db 356 ThrGlyThrGlyAlaGlyAlaGlyAlaCysThrThrThrCysAla----- 370
QY 992 TTCGGAGCTGAAGAGGTGCCATTGAGGAGCTGTACGAGAGTGTGAGGAGTGTGGCAGCTGT 1051
Db 371 -----ThrAlaGlyCysCysThrThrAlaGlyGlyCys 381
QY 1052 TCGCGAGGCGTGCACCCGCGCATTTGAGGAGCTGTACGAGAGTGTGAGGAGTGTGGCAGCTGT 1111
Db 382 AlaGlyAlaAlaAlaThrThrGlyAlaGlyCysCys-----Ala 394
QY 1112 TGTCCAAACCGACGACCAACTTCTGTGTCACAGCGCTCTGTGTACTTCCAGCAGCGCTGT 1171
Db 395 CysThrGlyThrAlaThrThrThr-----CysCysThrGlyThrGlyCysThrCys 412
QY 1172 ACTACAGGCGGCGATGGCAAGCTGTGTGG----- 1204
Db 413 AlathrCysAlaGlyCysThrAlaGlyAlaGlyAlaGlyAlaAlaAlaAlaAlaAlaThr 432
QY 1205 TGCTGCAAGTGCCTGGCGGTGTGGAGTGGCAAGACGCTCAAGCGCTCGCCCAAGC 1264
Db 433 CysCysAlaThrThrAlaCysCysAlaGlyGlyAlaThrGlyAlaAlaAlaAlaAlaGlyAla 452
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Db 453 AlathrAlaThrThrThrAlaThrAlaAlaGlyAlaThr----- 466
QY 1325 AGAAGCGGCCCAAGCCCGCTGTGTGGC-----TGTTCTCAAGT 1363
Db 467 ---ThrGlyGlyAlaAlaAlaCysAlaAlaAlaGlyGlyAlaAlaThrCysThrAlaCys 485
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QY 1424 AGCAGTACCGCTGATCAAGCGGAGCGCATCCCATTTGAGAACTATACATCCGGCGCACCA 1483
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QY 1538 ---ACTGCTCACCAGGTTCTGCGCGAACAATGCTGCCACCTACCTGCGCGAGGGGG 1594
Db 538 AlaAlaAlaGlyCysAlaGlyThrCysAlaGlyThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 557
QY 1595 CTTGCGCCACCTCAAGAGTGGCGTGGGCAACCTGACCGTCTCCACCAACTCTTCA 1654
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QY 1655 TGGAGGAGCTCAAAAGCGCGCACCTACACCAAGGTGATTCTGATGACCAACCGTGGACTGGC 1714
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RESULT 14
US-10-137-873A-219
; Sequence 219, Application US/10137873A
; Publication No. US20060084138A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Befesini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330P1C149
; CURRENT APPLICATION NUMBER: US/10/137,873A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-873A-219

Alignment Scores:
Pred. No.: 5,53e-09 Length: 1076
Score: 267.00 Matches: 121
Percent Similarity: 33.7% Conservative: 52
Best Local Similarity: 23.5% Mismatches: 223
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QY 542 TGAGCGCAAGTAGACCTGCCCCCTGCGCCAGATGCTGCTGGTGGCGGCTTCTTCTTCTGGC 601
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QY 602 GATCGATCTTCGACATCGACAACATTGACATCGSCCGCGCGCGCTTACCTCGGAGC 661
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Db 271 -----GlyThrCysAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 287
QY 722 TGGCGGCC-----CCTACTACGTGTGATTGGCGCGCTGCGCGCGCTGCGCGCGTTG 766
Db 288 CysThrThrCysThrGlyThrCysCysThrThrCysThrThrCysAlaAlaThrGlyGlyAla 307
QY 767 GCCACGCCCTGCACGAGGCGGTGGAGCGCGCGCGCGCATGTTCCCGCCACCTTCTCTGT 826
Db 308 AlaGlyAlaCysGlyThrThrThrThrThrGlyThrGlyThrCysAlaAlaAlaCysThrGlyCys 327
QY 827 ACAGCAGTGTGGGAGACCCCGAGCGCGGATATGAGAGTGATGAGAGATCAACCCCAAGG 886
Db 328 AlaAlaThrThrGlyCysAlaAlaAlaGlyCys----- 338
QY 887 ACAGGTGTGACCTGACCTGACGTAGCGCGCGCTGCAATGCTGAACTGCTGGTGCAGG----- 943
Db 339 ThrGlyCys-----AlaAlaGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 355
QY 944 -----GGCGCGCGCAGGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 991
Db 356 ThrGlyThrGlyGlyAlaGlyAlaCysThrThrThrThrThrCysAla----- 370
QY 992 TTCTGGAGCTGAAGAAGGTGGCCATTGAGAGCTGGAGTGTGAGAGAGTGTGGAGCTGT 1051
Db 371 -----ThrAlaGlyCysCysCysCysCysCysCysCysCysCysCysCysCysCysCysCys 381
QY 1052 TCGCGGAGGGGTGCACCGCGCATTTGAGGAGCTGTACGAGAAAGCTGCGCGCCCTTCC 1111
Db 382 AlaGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 394
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382 AlaGlyAlaAlaAlaThrThrGlyAlaGlyCysCys-----Ala 394
QY 1112 TGTGCAAAACCGACCAACTTCTGGTCCAAAGCGCTCTGTACTTCCAGACGCGCTGT 1171
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
395 CysThrGlyThrAlaThrThr-----CysCysThrGlyThrGlyCysThrCys 412
QY 1172 ACTACGAGGCGGCATGGCGAAGCTGTGCTGG----- 1204
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
413 AlaThrCysAlaGlyCysThrAlaGlyAlaGlyAlaGlyAlaThrGlyAlaAlaAlaThr 432
QY 1205 TGTCTCAGTGCCTGCGCGCTGTGGTGGAGTGGGCAAGACCGTCAAGCGCTCGCCCAACG 1264
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
433 CysCysAlaThrThrAlaCysCysAlaGlyGlyAlaThrGlyAlaAlaAlaGlyAla 452
QY 1265 CGCCCAATCGAGAGAGAGCGCGCTGTGTGGACAGCAATGCTCATCCACTTCGTGA 1324
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453 AlaThrAlaThrThrThrAlaThrAlaGlyGlyAlaThr----- 466
QY 1325 AGAAGCGGCCCAAGCGCTGGTGGC-----TGTTCTCAAGT 1363
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
467 ---ThrGlyGlyAlaAlaAlaCysAlaAlaGlyGlyAlaAlaThrCysThrAlaCys 485
QY 1364 TCGTAGCGCTGCTCTTCAACAGCGCTGTGTGGTTCGGCGCGCTGCCGGCA 1423
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486 AlaAlaAlaGlyCysCysAlaThr-----CysAlaGlyThrGlyAlaAlaCysThrGly 503
QY 1424 AGCAGTAGCGCTCATNAGCGGACGGCATCCCATTTGAGAACTACATCCGCGGCACCA 1483
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504 GlyAla-----ThrAlaThrThrCysThrCysThrThrCys 517
QY 1484 TGGACGGCGTGGCGAGAACTCGCACGCTGCGCAGCAGCAACTACTTCTACTACA----- 1537
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
518 CysThrGlyGlyAlaThrThrAlaAlaAlaAlaAlaThrThrAlaThrThrGlyGly 537
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538 AlaAlaAlaGlyCysAlaGlyThrCysAlaGlyThrAlaAlaAlaCysCysAlaAla 557
QY 1595 CTTTGGCCACCTCAAGAGTGGGTGGTGGACACCTGACCGCTCCACCAACTTCTTCA 1654
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
558 GlyCysCysAlaAlaGlyThrAlaCysAlaThrThrGlyAlaThrThrThrAla--- 576
QY 1655 TGGAGGAGCTCAAAGCGGCACCTACACCAAGGTGATTCTGATGGACCACTGGACTGGC 1714
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
576 ----- 576
QY 1715 TGGATATGCCGTGCCCAACGAGCTGGCGAGTGCCTGGCCAAAGCAGGTTCGCGGGCG 1774
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
577 -----CysAlaGlyThrThrAlaThrThrThrThrGlyAlaAlaAlaThrAlaCysAla 594
QY 1775 GCATCGTCATCTGGCGCT-----CCGCTCCCTCAGCCCGC 1810
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
595 AlaThrAlaAlaGlyAlaAlaCysThrGlyCysThrAlaGlyAlaAlaAlaThrAlaThr 614
QY 1811 CCTAGCGGAGCTGATCCAGAAGGGGCTTCGACGTGCGCTGCATCCGCGCGCCACTC 1870
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
615 GlyThrThrThrAlaThrAlaAlaCysAlaGlyThrCysThrAlaThrThrCysThr 634
QY 1871 AGGCTACATGGCGCGCTCAACATGTACAGCTCCTCTACA 1912
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
635 ThrThrThrAlaAlaAlaAlaAlaCysThrThrThrThrThrThr 648
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Search completed: May 5, 2006, 07:58:52
Job time : 75.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 07:45:05 ; Search time 26 Seconds
(without alignments)
2060.532 Million cell updates/sec

Title: US-10-620-914-45
Perfect score: 3463
Sequence: 1 MGSGRDGPASYTKNFSLE.....RVNMYSSPYMARRGAKKDN 648

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	352	10.2	310	2	US-09-248-796A-21233
2	158	4.6	222	2	US-09-248-796A-26335
3	121	3.5	212	2	US-09-107-532A-7254
4	118	3.4	329	2	US-09-902-540-16360
5	111	3.2	195	2	US-09-583-110-4761
6	111	3.2	198	2	US-09-107-433-4622
7	108.5	3.1	706	2	US-09-252-991A-24766
8	107	3.1	255	2	US-09-667-373-2
9	107	3.1	255	2	US-10-305-413-2
10	104.5	3.0	677	2	US-09-489-039A-13088
11	103.5	3.0	1070	2	US-09-107-532A-3716
12	101.5	2.9	663	2	US-09-711-164-332
13	99.5	2.9	471	2	US-08-994-689C-1
14	98.5	2.8	555	2	US-09-134-078-24
15	98.5	2.8	2636	2	US-09-252-991A-25753
16	97.5	2.8	464	2	US-09-134-001C-3488
17	97.5	2.8	471	2	US-08-994-689C-21
18	97	2.8	2209	2	US-10-017-754-1903
19	96.5	2.8	555	2	US-09-252-991A-28313
20	96.5	2.8	2470	2	US-08-265-967C-2
21	96.5	2.8	2470	2	US-08-305-790B-3
22	96	2.8	717	2	US-09-248-796A-18993
23	95.5	2.8	459	2	US-09-949-016-7329
24	94	2.7	480	2	US-09-438-185A-934
25	93.5	2.7	445	2	US-09-252-991A-17629
26	93.5	2.7	471	2	US-09-391-104-25
27	93.5	2.7	475	2	US-09-248-796A-15861

28	93.5	2.7	480	2	US-09-949-016-10560	Sequence 10560, A
29	93.5	2.7	590	2	US-09-489-039A-10743	Sequence 10743, A
30	92	2.7	574	2	US-09-605-703B-254	Sequence 254, App
31	92	2.7	1036	2	US-09-489-039A-10266	Sequence 10266, A
32	91.5	2.6	341	2	US-09-538-092-634	Sequence 634, App
33	91.5	2.6	681	2	US-09-248-796A-16367	Sequence 16367, A
34	91	2.6	749	2	US-10-104-047-2622	Sequence 2622, Ap
35	90.5	2.6	504	1	US-08-645-900A-1	Sequence 1, Appli
36	90.5	2.6	504	1	US-08-882-238A-1	Sequence 1, Appli
37	90.5	2.6	504	1	US-08-667-790A-1	Sequence 1, Appli
38	90.5	2.6	504	2	US-09-220-459-1	Sequence 1, Appli
39	90.5	2.6	504	2	US-08-938-689A-32	Sequence 32, Appli
40	90.5	2.6	504	2	US-08-548-568B-1	Sequence 1, Appli
41	90.5	2.6	504	2	US-08-822-999-3	Sequence 3, Appli
42	90.5	2.6	504	2	US-09-056-285A-8	Sequence 8, Appli
43	90.5	2.6	504	2	US-09-306-828-32	Sequence 32, Appli
44	90.5	2.6	504	2	US-09-952-464A-8	Sequence 8, Appli
45	90	2.6	500	2	US-09-543-681A-6847	Sequence 6847, Ap

ALIGNMENTS

RESULT 1

US-09-248-796A-21233
; Sequence 21233, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21233
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21233

Query Match		10.2%	Score 352;	DB 2;	Length 310;
Best Local Similarity		29.6%	Pred No. 3.1e-30;		
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QY	144	LITFSYSLTMI	PPFHNVIDQACSYLSQDGLVGVDYFVS	-----GKYD----	LPLRQMP 193
Db	3	LITFSYSLSMIPT	NAADNAVSKLDMGIIATVDFGIQSSDTS	MGRI	TGGLVNRDIP 62
QY	194	WSRFFWRSIF	DNIDIGPERRAYLEOKLERVNEQNTQ	-----GSI	PVPMRAPPYWI 249
Db	63	WILNFWRWF	EADKVFLDSSRRNYLFKFTVKLSYNKALGKI	-----PYIWI	114
QY	250	GRLPSVGHAL	HEE-----RVERPPMPFPPT	-----	273
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QY	274	-----	FLYTQSMEDPEPDMVMEINPKD	TVLT	TSGGCNCL 309
Db	175	YYQKEYWR	VYDEMPLVEQPKQYIYAFTWED	PRE	DHKLNFSDTVAITSAGDNIL 234
QY	310	NL--LVQ	GAGVSDCNPAQSALLEKKVAIQ	LEF	EDVWQLFGEVHPRIEELYEKL 367
Db	235	SYASLPT	PPKKIHADVNLNPCQHILLEKL	AS	FRCLSQEQIWSMFGEGKIENFNDLLIDL 294
QY	368	APFLSQT	SHNFWSKRLWYFQH 388		
Db	295	APHSSNA	-----FQH 305		

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RESULT 2
US-09-248-796A-26335
; Sequence 26335, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26335
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26335

Query Match          4.6%; Score 158; DB 2; Length 222;
Best Local Similarity 35.1%; Pred. No. 9,7e-09;
Matches 34; Conservative 20; Mismatches 19; Indels 24; Gaps 3;

QY 51 LESFYGPQAAAF-----AARLAERSNLIWDLGGGTGTGVNDMMADYI 92
DB 123 LESFYKNQAHYDNTREFLLKGRQCLRLAISHLPKXKDLIWDIDGGTGSNIEFMDBIS 182
QY 93 DLAK-FKSIYVVDLCHSLCEVAKKAKA-----KGWK 123
DB 183 KISENFKAVYLDLSPSLCEVAKARFESHDLTPRDWK 219

RESULT 3
US-09-107-532A-7254
; Sequence 7254, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7254:
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SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...212
SEQUENCE DESCRIPTION: SEQ ID NO: 7254:
US-09-107-532A-7254

Query Match          3.5%; Score 121; DB 2; Length 212;
Best Local Similarity 30.6%; Pred. No. 0.00013;
Matches 33; Conservative 23; Mismatches 44; Indels 8; Gaps 3;

QY 73 IWDVLGGGTGVNDMMADYIDLAKFKSIYVVDLCHSLCEVAKKAKAGWKNVQVVEADA 132
DB 53 VLDYGGGTGLVSLPLAE-----RFKELIIADASETMLKMAEEKIQADLKNVRTIHADA 107
QY 133 -CFAPPEGTATLITFSYSLTMIPPHNVIDQACSYLSQDGLGVADF 179
DB 108 SVERF--PAVQANLILLSLVLLHIPDTENILTKLYEILLAPGGQLIIVDF 153

RESULT 4
US-09-902-540-16360
; Sequence 16360, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16360
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16360

Query Match          3.4%; Score 118; DB 2; Length 329;
Best Local Similarity 21.8%; Pred. No. 0.00059;
Matches 81; Conservative 37; Mismatches 121; Indels 132; Gaps 16;

QY 264 VERPPMFPPTFLYTSQSWEDPEPDMVMEINPKDTVLTITSGGCNALLLVQ-GAGQVVSV 322
DB 6 VSTPEPL---RLKFAVREDAALELALVERTRARAVLTIVASGGCTLLTLARRHPALELVGF 62
QY 323 DCNPAQSALLELKKVAIQQL-----EPEDVWQLFG-----EGVHPRIEELYEKKLAPFL 371
DB 63 DFNPRQLAHVREKAEGLRLPLARYSDAEDAAALNQRGEFGLFRTLRRFIEEFVAP-- 120
QY 372 SQTSHNFWSKELWYFQHGLYYQGGMGKLCWLQCLAVVLGLGKTVKRLANAP-TMEEORR 430
DB 121 ---AHE-----LAAPF-----APATTASORR 138
QY 431 LWDNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAVLMFGGVPKGQYALIKADGIPIENY 490
DB 139 -----EACARWFAFELAAAPLEN- 164
QY 491 IARTWDGVAENSHVRKQNY-----FYNCLTKGFLRDNCTYLR 529
DB 165 ---TMFGPAATQHAEPGSGYPGYFOAVFERGLQREDAPRNPFLQHVLLGRYLRDAPAYLR 221
```

```
QY 530 -EAEFA-TLKSGVDNLTSTNFFMEELKARTYTKVILMDHV-DWLDMPVANELAECLAK 586
; . . . . .
Db 222 ABGPLALTIVQGSLEDPVRLDRF-----DVLSLNFIDWSEDAVAEAGVILAR 270
; . . . . .
QY 587 QVAPGGIVWR 597
; . . . . .
Db 271 EARFCAVLIR 281

RESULT 5
US-09-583-110-4761
; Sequence 4761, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4761
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4761

Query Match 3.2%; Score 111; DB 2; Length 195;
Best Local Similarity 28.0%; Pred. No. 0.0014;
Matches 40; Conservative 28; Mismatches 59; Indels 16; Gaps 6;

QY 46 DHAARLESFYGPQ---AAAFARLAR-----SNLIWVDLGGGTGENVDMADYIDLAK- 96
; . . . . .
Db 4 DFNHKAETFDSPKNIPLANLVCQAVEKQIDILSKVILDFGGGTG----LLA--LPLAKQ 57
; . . . . .
QY 97 FKSIVVDLCHSLCEVAKKAKGKNVQVVEADACQAFAPGETATLITFSYSLTMIPP 156
; . . . . .
Db 58 AKSVTLVDISEKMLEQARLKEQQAIRKIQLEQDLPK-NPLEKEFDCLAVSRVLHMPD 116
; . . . . .
QY 157 FHNVIDQACSYLSQDLGVADF 179
; . . . . .
Db 117 LDAALSLFHQHLKEDGKLIADP 139

RESULT 6
US-09-107-433-4622
; Sequence 4622, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:

QY 42 KKGDHAAARLESFYGPQAAAFARLARSN-----LIWVDLGGGTGENVDMADYI 92
```

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; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4622:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...198
; SEQUENCE DESCRIPTION: SEQ ID NO: 4622:
US-09-107-433-4622

Query Match 3.2%; Score 111; DB 2; Length 198;
Best Local Similarity 28.0%; Pred. No. 0.0015;
Matches 40; Conservative 28; Mismatches 59; Indels 16; Gaps 6;

QY 46 DHAARLESFYGPQ---AAAFARLAR-----SNLIWVDLGGGTGENVDMADYIDLAK- 96
; . . . . .
Db 7 DFNHKAETFDSPKNIPLANLVCQAVEKQIDILSKVILDFGGGTG----LLA--LPLAKQ 60
; . . . . .
QY 97 FKSIVVDLCHSLCEVAKKAKGKNVQVVEADACQAFAPGETATLITFSYSLTMIPP 156
; . . . . .
Db 61 AKSVTLVDISEKMLEQARLKEQQAIRKIQLEQDLPK-NPLEKEFDCLAVSRVLHMPD 119
; . . . . .
QY 157 FHNVIDQACSYLSQDLGVADF 179
; . . . . .
Db 120 LDAALSLFHQHLKEDGKLIADP 142

RESULT 7
US-09-252-991A-24766
; Sequence 24766, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24766
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24766

Query Match 3.1%; Score 108.5; DB 2; Length 706;
Best Local Similarity 19.6%; Pred. No. 0.026;
Matches 94; Conservative 54; Mismatches 170; Indels 161; Gaps 25;

QY 42 KKGDHAAARLESFYGPQAAAFARLARSN-----LIWVDLGGGTGENVDMADYI 92
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```
Db 174 REGELLORCAERGPEIAACAPLAERLQACQSVVERVALM--LAAGTGELLRLVGPRE 231
Qy 93 DLAKFSIYVVDLCHSLCEVAKKAKAGWKNV--QVVEADACQFAPPEGT-----A 142
Db 232 HLVRAREYVP-----EVERPLARFASWYELFPRSSGDPTR-----HGTFFDVIRRLP 279
Qy 143 TLITFSYSLTWIPPHNV-----IDQACSYL--SQDG-----172
Db 280 QIAWGFVLYFPPIHPITGRTHKGRNNSLRABADPGSPYAIGSEDGGEAIIHPELGDR 339
Qy 173 -----LVGV-----ADFYVSGKYDLP--LROMP--WSRFFFWR-----SI 203
Db 340 EDFRLLVAVREHGMELALDAIQCSPDHPWLRHPGM---FANRPDGLRYAENPPPKY 396
Qy 204 FDIIDIDIGPERRAYLEOKLRVWEQNTQGSIPVY-----PWLK-APYVVI-- 249
Db 397 EDIVNVDF-----YAEQALPSLWEALRDVVVLGWEQGVTLFRVDNPHTKPLPFEWMLIA 450
Qy 250 ---GRLPSVGHALHEEVERPPM-----PPTFLY-----TQSW 280
Db 451 EVRGHPQV--IFLSEAFTRPAMMARLKGVGFOSQSYTYFTWRNDKQELAEYFABELNOPPW 508
Qy 281 ED---PEPDMVMEINPKDVTLTITSGGCNALNLLVOGAG-----QVSVSDCNPAQS 329
Db 509 RDCVRPNFVNTPDINPWFLOSRGPGFLIRAAATWGLWGMVSGFELCEAAALPKKE 568
Qy 330 ALLELKVAIQOLEFEDVWQFEGVHPRIELEYEK--LAPFLSQTSNFWSKRLMYWF 386
Db 569 BYLDEKYLQRPDYQAPGNVAE--IARLNIRRENPAIQLHLGFQAYNAWNRILYF 625

RESULT 8
US-09-667-373-2
; Sequence 2, Application US/09667373
; Patent No. 6524840
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6524840el Human Endothelin Converting
; TITLE OF INVENTION: Enzyme-Like Proteins and Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/667,373
; PRIOR FILING DATE: 2000-09-22
; PRIOR FILING DATE: 2000-09-22
; PRIOR FILING DATE: 1999-09-24
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-667-373-2

Query Match 3.1%; Score 107; DB 2; Length 255;
Best Local Similarity 22.9%; Pred. No. 0.0065;
Matches 53; Conservative 20; Mismatches 68; Indels 90; Gaps 11;

Qy 213 PERR-AYLEOKLERVWEQNTQGSIPYVWLRAPYVWIGRLPSVGHALHEEVERPPMFP 271
Db 14 PERNCYGREVE---YWDQRYQGAADSAP-----YDMFGDSSFALL-----52
Qy 272 PTFLYTQSWEDPEPDMVMEINPKDVTLTITSGGCN-----ALNLLVQAGOVSVDCNPA 327
Db 53 -----EP-----ELRPEDRILVL---CGNSALSLEYELFGGFPNVTSDYSSV 92
Qy 328 QSALLELKVAIQOLEFE-----DVMQLFGEVGH 356
Db 93 VVAAMQARYAHVPQLRWETMDVRKLDPFPSASFDVVLSEKGTLDALLAGERDPWTVSSEGVH 152
Qy 357 PRIEELVE--KKLAP---FLSQTS-----HNFWSKRLMYFOHGLYYQG 394
Db 153 TVDQVLSEVSRVLPVGGGRFISMTSAAHPFRTRHYAQAYYGWSLRHATYVSG 203

RESULT 10
US-09-489-039A-13088
; Sequence 2, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
```

```
Db 93 VVAAMQARYAHVPQLRWETMDVRKLDPFPSASFDVVLSEKGTLDALLAGERDPWTVSSEGVH 152
Qy 357 PRIEELVE--KKLAP---FLSQTS-----HNFWSKRLMYFOHGLYYQG 394
Db 153 TVDQVLSEVSRVLPVGGGRFISMTSAAHPFRTRHYAQAYYGWSLRHATYVSG 203

RESULT 9
US-10-305-413-2
; Sequence 2, Application US/10305413
; Patent No. 6835564
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6835564el Human Endothelin Converting
; TITLE OF INVENTION: Enzyme-Like Proteins and Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/305,413
; PRIOR FILING DATE: 2002-11-25
; PRIOR FILING DATE: US/09/667,373
; PRIOR FILING DATE: 2000-09-22
; PRIOR FILING DATE: 1999-09-24
; PRIOR FILING DATE: US 60/176,689
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-305-413-2

Query Match 3.1%; Score 107; DB 2; Length 255;
Best Local Similarity 22.9%; Pred. No. 0.0065;
Matches 53; Conservative 20; Mismatches 68; Indels 90; Gaps 11;

Qy 213 PERR-AYLEOKLERVWEQNTQGSIPYVWLRAPYVWIGRLPSVGHALHEEVERPPMFP 271
Db 14 PERNCYGREVE---YWDQRYQGAADSAP-----YDMFGDSSFALL-----52
Qy 272 PTFLYTQSWEDPEPDMVMEINPKDVTLTITSGGCN-----ALNLLVQAGOVSVDCNPA 327
Db 53 -----EP-----ELRPEDRILVL---CGNSALSLEYELFGGFPNVTSDYSSV 92
Qy 328 QSALLELKVAIQOLEFE-----DVMQLFGEVGH 356
Db 93 VVAAMQARYAHVPQLRWETMDVRKLDPFPSASFDVVLSEKGTLDALLAGERDPWTVSSEGVH 152
Qy 357 PRIEELVE--KKLAP---FLSQTS-----HNFWSKRLMYFOHGLYYQG 394
Db 153 TVDQVLSEVSRVLPVGGGRFISMTSAAHPFRTRHYAQAYYGWSLRHATYVSG 203

RESULT 10
US-09-489-039A-13088
; Sequence 2, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
```



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; SEQ ID NO 13088
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13088

Query Match          3.0%; Score 104.5; DB 2; Length 677;
Best Local Similarity 21.4%; Pred. No. 0.068;
Matches 63; Conservative 29; Mismatches 91; Indels 111; Gaps 15;

QY 235 IPVPMRLAPYVYVWIGRLPSVGHALH-----EERVERPPMFP--PTFLYTQSWEDPE 284
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 193 IEVSPGVGVYWIWALQSLGIGITLTGINFVVIKKRAQMTWFKVPF-----SWASLC 248
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 285 PMEVMBEINPKDVTVLITSGCCNALNLLVOGAGQVSDCNPAQSALLELKKVAIOOLEF 344
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 ANILIIASFP--ILTVT-----IALLTLDRYLGTHFT 279
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 ED-----VWOLFGEVHPRIEELYEKKLAPF--LSQTSHPNFWSKLWYFQHG 391
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 280 NDMGNGMMYINLIW-AWG---HP---EVYILVLPVEGVSEIATFSKRLF----- 325
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 392 YQSGMGKLCVWLOCLAVV-----LGLGKTVKRLANAPTEBQRRLWDSNMLIHF 440
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 326 ---GYTSLWATVCITVLSFIVLHLHFTTWGAGANVNAFFGITM-----IIA 370
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 441 VKQPKPLWLVFKFVSLVLFNKAVLW-----FGG-----GVPGKQYAL 479
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 371 IPTGVKIFNLFTMYQGRIVFNSAMMTIGTIVTFSVGGTGVLLAVPGADFVL 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-107-532A-3716
; Sequence 3716, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1070 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```
Db 276 INLIW-ANG---HP---EVYIILPVFGVFSEIAATFSKRLP-----GVTSLVM 318
QY 402 VLOCLAVV-----LGLGKTVKRLANAPTMEEORRLWDSNMLHFVKNQGPKLPLW 450
Db 319 ATVCITVLSFVWLHHFFTMGAGANVNAFFGITTM-----IIAIPTVGVKIFNW 366
QY 451 LFKVKVSLVLFENKAVLW-----FGG-----GVPGKQVAL 479
Db 367 LFTMTQGRIVFHSAMLWTIGFIVTFSVGGMTGVLLAVPGADFVL 410

RESULT 13
US-08-994-689C-1
; Sequence 1, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Lorán
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greán, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-994-689C-1

Query Match 2.9%; Score 99.5; DB 2; Length 471;
Best Local Similarity 18.4%; Pred. No. 0.13;
Matches 100; Conservative 61; Mismatches 159; Indels 223; Gaps 27;

QY 51 LESFVGP-----QAAFAAFLAERSNLIVDLGGGTGEN-VDMM-----ADYIDLA 95
Db 43 LRSYHYHTNLGAILKENAASSMTERLRMSQSFGLVETGKDDNTLDVNMKPRCGVVDVG 102
QY 96 KFKSI-----YVVDLCHSLCEVAKKAKAGKGNVQVVEADACQFAPP 138
Db 103 EYNVFPRTLKWSKMLTYRIVNYTFDMTHSEVEKAFKA-FKVNSDVTPLN-----152
QY 139 EGTATLITFSVSLTWIPPHNVVIDQACSVLSODGLVGVDIFY-VSGKYDLPURQMPWRR 197
Db 153 -----FTRLHDGIADIMISFGIKEHGDFYFPDGPGLLAHAFPPGPN 194
```

```
QY 198 FFWRSIPDIDNIDIGPERRAYLEQKLERVWEQNTQGSIPYVWMLRAPYVYVWIGRLPSVGH 257
Db 195 YGGDAHFDD-----ETWSSSKG-----YNLFVAHAHEFGH 226
QY 258 ALHEERVERPP--MPPPTFLYTQSWEDPEPDMVEYMEI-----NPKDVTVLTLTSG 304
Db 227 SLGLDHSKDPGALMF-PIYTYTGKSHFMLPDDDVQGIQSLYGPGEDEDENPKH-----277
QY 305 GCNALNLLVQAGAGVSVDCNPAQS--ALLLKKVAIQOLEFED--VMQLFGEVHP---357
Db 278 -----PKTPDKCDPSLSLDAITSLRG---ETMIFKORFFWRL-----HPOOV 316
QY 358 -----RIEELYERKKLAPFLSQTSHNFWSKLWYFOHGLYQGGMGKLCW 401
Db 317 DAELFLTKSFWPELPNRIDAAYE-----HPSHDL-----IFIFR-----GRKFW 355
QY 402 VLOCLAVV-----LGLGKTVKRLANAPTMEEORRLWDSNMLHFVKNQGPKLPLWLF 452
Db 356 ALNGVDILLEGYPKKISLGLPKVKKISAA-----VHPEDTG-----392
QY 453 VKFVSLVLFNKAVLW---FGGVFGKQYALIKADGIPNIENYIARTMDGVAENSHVKQNY 509
Db 393 ----KTLFSGNQVWRVDDTNHIMDKOYPRLIEEDFP---GIGDKVDAYE-----KNGY 440
QY 510 FYY 512
Db 441 IYF 443

RESULT 14
US-09-134-078-24
; Sequence 24, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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US-09-134-078-24

Query Match 2.8%; Score 98.5; DB 2; Length 555;

Best Local Similarity 18.9%; Pred. No. 0.23;

Matches 111; Conservative 74; Mismatches 166; Indels 237; Gaps 31;

QY 111 EVAKKAKAK-----GKQVQVVEADACQAPPEGTATLITFSYSTMTIPPPHNVID- 162

DB 50 EYLRKAPEKVLVNNQWQGPCRVV--DAFSKPEIDP--NMYTASVVP---DVLER 101

QY 163 --QACSYSODGLV-GVADFYVSGKVDLPLROMPSRRFFWRSIFDIIDNIDIGP-ERRAY 218

DB 102 NLOSDYFAEBEKVYG-----FLSSKIAHPFFRAVEDGELVAYLEYDFVDFDVPVLEPLVV 157

QY 219 LEOKLERVMEQNTQGSIPYVWMLRAPPYVWIGRLPSVGHALHEEREVERPPFPPT----- 273

DB 158 LED-----PNTPLLEKAYELVGM-----ENNARVPKHTPTPGWCSW 193

QY 274 --FLYTQSWEDPEPM-----EVMENPK-----DTVLTLTSGGCNALLLVQAG 317

DB 194 YHYFDLTLTWEETLKNLKLAKNPPFPFVQIDDAYEKDIDGWLVT-----RG 238

QY 318 QVSVSDCNPAQSALLEKKAIVAIQOLEPEDVM-----QLFGEVHPR--IEELYEK 365

DB 239 DFPSE-----EMAKVIAENGFIGIWTAPFSVSETSDVFN--HPDWVKNENGP 287

QY 366 KLAPFLSOTSHNFWSKRLMYFQHGLYQGGMGKLCWVLQCLAVLGLGKTVKRLANAPTM 425

DB 288 KWA-----YRNWNKKIY-----ALDLSK-----HVRKQ 507

QY 426 EQORLSDNSMLIHVFKNGKPLVWLFVKFVSL-----VLFKNAVLPFGGVPKGQYALIK 481

DB 306 -----DEVNLNLFDFLSSLRKMGYFKIDPLFAGAVPGER-----K 342

QY 482 ADGIPIENY-----IARTMDGVAENS-----HVRKQ 507

DB 343 KNITPIQAFRGIEITIRKAVGEDSFILGCGSPLLPVAGCVDMGRIGPDTAPFWGSHIEDN 402

QY 508 -----NYFYNYCLTGKFLRD-----NCPTYL-----REAFATLKSQVVDNLTVS 547

DB 403 GAPAARWALRNALTRYFMDHDFWLNDDPCLILREKTDLTOKERELYSYTCGLDNLMIIE 462

QY 548 TNFMFEELK-ARTYTKVILMDHVDWLD--MPVANELAECLAKQVAPGG 592

DB 463 S-----DDLSLVRDHGKVKLTKETLELLGGRPRVQNMSEDRLYEIVSSG 506

RESULT 15

US-09-252-991A-25753

; Sequence 25753, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252.991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25753

; LENGTH: 2636

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-25753

Query Match

Best Local Similarity 20.6%; Score 98.5; DB 2; Length 2636;

Matches 124; Conservative 68; Mismatches 231; Indels 179; Gaps 29;

QY 127 VVEADACQAPPEGTATLITFSYSTMTIPPPHNVIDQACSYLSQDGLGVADFYVSGKVD 186
DB 379 VLGAQHODLPEFLVEAFKVERSLSHSPFLQVMYNHQPLVADIEALDSVA-----G 430
QY 187 LPLQMPWSRRFFWRSIFD--IDNIDIGPERRAYLE-----OKLERVWE----- 228
DB 431 LSPQOLDWKS-----TTQFDLSLDYVEKGRGRLYAALTATDLEFARTVERMARHWNLLRG 487
QY 229 --QNTQGSIPYVWMLRAP--YVWIG-----RLPSVGHALHEEREVERPPFPPTFLY 276
DB 488 MLENQASVDSLPMLDABERYQLLEGWNTAAEYPLQRGVHRLFEEOVERTPTALAF- 546
QY 277 TQSWEDPEPMVEVMEINPKOTVL--TLTSGGCN-----ALNLLVQAG 317
DB 547 -----GEERLDYAELENRRANRLAHALITERGVGADRLGVAMERSIEMVVALMAILKAGG 600
QY 318 QVSVSDCN-PAQSALLEKKAIVAIQOLEPEDVMQL-FGEGVH-----PRIEELYEKKL 367
DB 601 AYVPVDPEYPERQAYMLEDGCVQLLSQSHLKLPLOAGVQVQVQVQVQVQVQVQVQVQV 659
QY 368 APFLSOTSHNFWSKRLMYFQHGLYQGGMGK-----LCWVLQCLAVLGLG 413
DB 660 -PDHLDGEN-----LAYVIYTSGSTGPKGAGNRHSALSNNRLCWMQO--AYGLGVG 708
QY 414 KTVKRLANAPTMESQORRLWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFKNKAVLWFGGG-- 471
DB 709 DTV-----LOKTPFSFDVS-----VMEF--FWPLMSGARLVVAAPGDHR 745
QY 472 VPGQYALIKADGIPNIENYIARTMDGVAENSHVRKQNYFYNYCLTGKFLRDNCPYLR 531
DB 746 DPAKLVELINREGVDTLHFVPSMLQAPLQDEDDVASCSTLKRIVCSGEAL-----PADAQOQ 801
QY 532 AFATLKSQVVDNLTVSTNFFMEEELKARTYTKVILMDHVDWLDM-----PVANEL 580
DB 802 VFAKLPOAGLYNLXGPT-----AAIDVTHWTCMEEGKDAVPIGRPIAN-- 845
QY 581 AECLAKQVAPGGIWIWSASLSP-PYABEL--IQAGFDVRCIRATQGYMDRVNMYSSFY 637
DB 846 ---LACYILDG-----NLEPVVGVVLGBELYLAG-----RGLARGYHORPGLTABRF 888
QY 638 MA 639
DB 889 VA 890

Search completed: May 5, 2006, 07:46:28

Job time : 28 secs

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OM protein - protein search, using sw model

Run on: May 5, 2006, 07:48:33 ; Search time 87 Seconds
(without alignments)
3112.108 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSGRDGRPASYYTKNFSLE.....RVNYSFYMARKGAKDN 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3463	100.0	648	4	US-10-620-914-45
2	891	25.7	752	5	Sequence 45, Appl
3	850.5	24.6	908	4	Sequence 7021, Ap
4	379.5	11.0	416	4	US-10-620-914-50
5	379.5	11.0	416	4	US-10-118-495-3
6	326.5	9.4	416	4	US-10-620-914-3
7	326.5	9.4	416	4	US-10-118-495-29
8	321	9.3	415	4	US-10-620-914-29
9	321	9.3	415	4	US-10-118-495-41
10	292.5	8.4	416	4	US-10-620-914-41
11	292.5	8.4	416	4	US-10-118-495-33
12	123	3.6	2284	5	US-10-620-914-33
13	123	3.6	2284	5	US-10-684-141-58
14	120	3.5	2284	5	US-10-810-486-58
15	120	3.5	221	4	US-10-118-495-35
16	119	3.4	2286	5	US-10-620-914-35
17	119	3.4	2286	5	US-10-684-141-54
18	112.5	3.2	672	4	US-10-810-486-54
19	111	3.2	198	5	US-10-282-122A-68178
20	110.5	3.2	298	5	US-10-617-320-4622
21	107	3.1	255	4	Sequence 4622, Ap
22	107	3.1	255	4	Sequence 38334, A
23	107	3.1	691	5	US-10-220-381-24
24	106.5	3.1	670	4	US-10-988-984-2
25	106	3.1	472	3	US-10-732-923-9665
26	106	3.1	472	3	Sequence 69771, A
27	106	3.1	472	4	US-09-974-238-120
					Sequence 120, App
					Sequence 186, App
					Sequence 201, App

28	106	3.1	472	4	US-10-468-406-2	Sequence 2, Appli
29	106	3.1	472	5	US-10-370-715B-256	Sequence 256, App
30	106	3.1	852	4	US-10-437-963-108559	Sequence 108559,
31	106	3.1	2039	4	US-10-369-493-21994	Sequence 21994, A
32	104.5	3.0	663	4	US-10-282-132A-59897	Sequence 59897, A
33	104.5	3.0	664	4	US-10-389-647-469	Sequence 469, App
34	104	3.0	225	4	US-10-118-495-42	Sequence 42, Appl
35	104	3.0	225	4	US-10-620-914-42	Sequence 42, Appl
36	103.5	3.0	1064	5	US-10-437-923-8191	Sequence 8191, Ap
37	103	3.0	908	4	US-10-437-963-132823	Sequence 132823,
38	101.5	2.9	663	3	US-09-815-242-10070	Sequence 10070, A
39	101.5	2.9	663	4	US-10-287-274-332	Sequence 332, App
40	101.5	2.9	663	4	US-10-282-122A-56452	Sequence 56452, A
41	101	2.9	652	4	US-10-282-122A-73132	Sequence 73132, A
42	101	2.9	679	4	US-10-282-122A-48489	Sequence 48489, A
43	100	2.9	323	4	US-10-437-963-162897	Sequence 162897,
44	99.5	2.9	471	4	US-10-375-884-1	Sequence 1, Appli
45	99.5	2.9	663	3	US-09-815-242-14080	Sequence 14080, A

ALIGNMENTS

RESULT 1
US-10-620-914-45
; Sequence 45, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; TITLE OF INVENTION: Klug, Rouven
; FILE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-45

Query Match 100.0%; Score 3463; DB 4; Length 648;
Best Local Similarity 100.0%; Pred No. 0;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSGRDGRPASYYTKNFSLEKLSMMKDDLTVLRLHMMFGSKGDDHAARLESFYGPQAA	60
Db	1	MGSGRDGRPASYYTKNFSLEKLSMMKDDLTVLRLHMMFGSKGDDHAARLESFYGPQAA	60
Qy	61	AFAARLAERSNLIWVDLGGGTGENVDMADYIDIAKFKSIYVDLCHSLCEVAKKAKAK	120
Db	61	AFAARLAERSNLIWVDLGGGTGENVDMADYIDIAKFKSIYVDLCHSLCEVAKKAKAK	120
Qy	121	GWKNVQVVEADACQAPPEGTATLITTSYGLTMTIPPPHNVIDQACSYLSQDLGVADVF	180
Db	121	GWKNVQVVEADACQAPPEGTATLITTSYGLTMTIPPPHNVIDQACSYLSQDLGVADVF	180
Qy	181	VSGKYDLPRLQMPNRRFFWRSIFDINIDITGPERRAYLEQKLRVWEQNTQGSIPYVPW	240
Db	181	VSGKYDLPRLQMPNRRFFWRSIFDINIDITGPERRAYLEQKLRVWEQNTQGSIPYVPW	240
Qy	241	LRAPYYWIGRLPSVGHALHEERVERPMPPTFLYTQSWEDPDPMVMEINPKDTVLT	300
Db	241	LRAPYYWIGRLPSVGHALHEERVERPMPPTFLYTQSWEDPDPMVMEINPKDTVLT	300
Qy	301	LTSGCCNALNLLVQAGQVSDCNPAQSALLEKKVAIQOLEFEDVWQLFEGVHPRIE	360
Db	301	LTSGCCNALNLLVQAGQVSDCNPAQSALLEKKVAIQOLEFEDVWQLFEGVHPRIE	360

QY 361 ELYEKKLAPFLSOTSHNFWSKRLWFOHGLYQGGMGKLCWVLOCLAVVLGKTVKRLA 420
DB 361 ELYEKKLAPFLSOTSHNFWSKRLWFOHGLYQGGMGKLCWVLOCLAVVLGKTVKRLA 420
QY 421 NAPTMEQORRLWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAIVLWFGGVPKGQYALI 480
DB 421 NAPTMEQORRLWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAIVLWFGGVPKGQYALI 480
QY 481 KADGIPINENYARTMDGVAENSHVRKQNYFYNYNCLTGKFLDNCPTYLREAAATLKSQV 540
DB 481 KADGIPINENYARTMDGVAENSHVRKQNYFYNYNCLTGKFLDNCPTYLREAAATLKSQV 540
QY 541 VDNLTVSTNFMEEELKARTYTKVILMDHVDMLDMPVANELAECLAKQVAPGGIVWRSAS 600
DB 541 VDNLTVSTNFMEEELKARTYTKVILMDHVDMLDMPVANELAECLAKQVAPGGIVWRSAS 600
QY 601 LSPPYAEILQKAGFDVRCIRBATOQYMDRVNMYSSFYMARRRKAKKON 648
DB 601 LSPPYAEILQKAGFDVRCIRBATOQYMDRVNMYSSFYMARRRKAKKON 648
RESULT 2
US-10-741-849-7021
; Sequence 7021, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7021
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-741-849-7021
Query Match 25.7%; Score 891; DB 5; Length 752;
Best Local Similarity 32.7%; Pred. No. 4.4e-80;
Matches 229; Conservative 98; Mismatches 232; Indels 142; Gaps 21;

QY 51 LESFYGPQAAAF-----AARLAERSNLIVDLGGGTGENVDMADYI 92
DB 70 LESFYKNOAHYDNTREFLLKRGQECRLAIASHLPKKKDLIWDIGGTGSGNIEPFMDEIS 129
QY 93 DLAK-FKSIYVVDLCHSLCEVAKKAKAGKQNVQVVEADACQAPPREGTATLITFSYSL 151
DB 130 KISENFKAVYLVDLSPLSCEVAKARFEAHETNVHVLVADACDFDIYDSADLITFSYSL 189
QY 152 TWIPPFHNVIDOACSYLSQDGLGVGVFVS-----GKYD-----LPLRQMPWSRRFPWR 201
DB 190 SMIPTFNAADINAVSKLDMEGIIATVDFGIQSSDTSMGRIINTVGLVNRDIPWILRNFWR 249
QY 202 SIFDIDNIDIGERRAYILEOKLERWEQNTQ-----GSIPYVPLREAPYVMIGRLPSVGH 257
DB 250 IWFADKVFLODSSRRNILEYKFGTVKLSNYSNKAIGKI-----PYIWIIGCDKSKSH 301
QY 258 ALHEE-----RVERPPMPFPT-----PIANQLEDIPISKGEAALINLQKNLPSPMYQKEYR 361
DB 302 TILERLNCLATESPVIATTTPIANQLEDIPISKGEAALINLQKNLPSPMYQKEYR 361
QY 274 -----FLYTSQWEDPEPDMVEINPKDVTULTLTSGGCNALNL--LVQG 315
DB 362 VYDEMNPBYQKNOYIYAFTWEDPREDHKLNFSTSDTTLVAITSGDNILSVASLPTP 421

QY 316 AGOVVSDCNPAQSALLLEKKVAIQOLEFEFDWOLFEGGVHPRIEELYEKKLAPFLSOTS 375
DB 422 PKKIHADVLDNLCQNHLELEKLASFRCISQEQIWSMFGEKTIENFNDLLIDTILAPHMSNA 481
QY 376 HNFWSKR--LWYFOHGLYQGGMGKLCWVLOCLAVVLGKTVKRLANAPTMEEQRR 430
DB 482 FOYWMDKGPKTFSKGLY--DTGFSRWALRLSYVFKVCGVSKYVBEELCAATTMEEQRL 538
QY 431 LWDNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAIVLWFGGVPKGQYALIKADGIPINEN 489
DB 539 IWEHLL-----KPT--LFNPFVVGSLLVGNPMFLWALGVSPANQAALM---GPSVIK 584
QY 490 YIARTMDGVAENSHVRKQNYFYNYNCLTGKFLDNCPTYLREAAATLTK-----SGVV 541
DB 585 YVDTLDFIIRKSMISNDNYFYNYNCLTGKFLDNCPTYLREAAATLTK-----SGVV 541
QY 542 DNLTVSTNFMEEELKARTYTKVILMDHVDMLDMPVANELAECLAKQVAPGGIV 595
DB 645 DNLRIHTDNLNEVFGRLKEKSITTAIIMDHMDWDFDPNGRDAINEIT-ALKRCLAPGGRVL 703
QY 596 WRSASLSPPYAEILQKAGFDVRCIRBATOQYMDRVNMYSS 635
DB 704 LRSASTKFWYLKTPKNLGFQEEENVVRQPGSSIDRVNMYAN 744
RESULT 3
US-10-620-914-50
; Sequence 50, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 50
; LENGTH: 908
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-620-914-50
Query Match 24.6%; Score 850.5; DB 4; Length 908;
Best Local Similarity 30.4%; Pred. No. 7.3e-76;
Matches 222; Conservative 105; Mismatches 235; Indels 169; Gaps 18;

QY 69 RSNLIWDLGGGTGENVDMADYIDLAK-FKSIYVVDLCHSLCEVAKKAKAGKQNVQV 127
DB 178 RRPDIWVDVGGGTGNIEAMAKFVNVSEFFKTVYLVDFSPSLCEVARKFARLWENVRV 237
QY 128 VEADACQFA-----PREGT-----ATLITFSYSLTWIPPF 157
DB 238 ICTDARKFRLDEYEDVDEGESGSDSPSLSGWGWETKPGRHAGAEILTMSYLSLMDY 297
QY 158 HNVIDOACSYLSQDGLGVGVADFYVSGKYD-----LPLRQMPWSRRFPWRISFDIDN 208
DB 298 FSIIDSLESLLAPHGLIAVDFYAGSKVDFTFRNYTGLMNRHVGYFARNEWRWSFDADR 357
QY 209 IDIGERRAYILEOKLERW-----EQNTQGSIPYVPM---LRAPYV-----247
DB 358 VSLFAPARDYLEYRFGTVLTVNARNNTLGAIPYIWLGLCKLPKPFSTSLPHEIVSHIDAI 417
QY 248 -----WIGR-----LPSVGHALH 260
DB 418 ATESPRSPRLVGKSSSATNALAFAGVGTAPEMRSKAFNTAIENISANLPLPSFFYQNH 477
QY 261 -----EERVRPMPFPPTFLYTSQWEDPEPDMVEINPKDVTULTLTSGGCNALNLVQ 314

Db 478 HWRIYYDDOLPKHTQFNDEYIYAFTHWEDSRVDRBELNLGPDVVLAI TSAGNNILSYLMO 537
Qy 315 GAGQVVSVCNPAQSALLEKKVAIQOEFEDVWOLFQEGVHPRIEELYEKKLAPFLSQT 374
Db 538 SPARVHAI DLNPAQNHLELKVASPTTLDYPDVWKIFGEGKHPDFRSLLSKLSPHLSGR 597
Qy 375 SHNFWSKLWYFQ---HGLYYQGGMGKLCWVLOCLAVVLGLGKTVKRLANAPTMEQR 430
Db 598 AFQYWLNAHIFTDPAGRLGYDTGSRVYAIRFRWISTLFFCRSAVRRLSLTPTLEGORS 657
Qy 431 LWDNMLHFVKNVGNPKPLVWLFVKVS-LVLPNKAVLWFGGVPGKQVALIKAD----- 483
Db 658 IYHTKI-----RPC--LLNRFVNGVLSSDAFLWSALGVKNQVAMHEADVHRSI 706
Qy 484 -----GPIENYIARTMDGVAENSHVRKQNYFYNYNCLTGKFLRDNCPYTLR 529
Db 707 SSSTTPSSKEKPSRAEAILHYTTSLDPVLSTSHLASDNPPYLVCLVGOYTRQCHPDYLS 766
Qy 530 EAAFATLKS-GVVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMP----- 575
Db 767 PAHSILSAGPAFDGLRIHTDIOEVLARFQFGTTLTVAVWDSMDWFDPPPEESKEGRG 826
Qy 576 VANELAECLAKQVAPGIVIVRSASISPPYAEILQKAGFVRCI-----RRATQGYMDRV 630
Db 827 KAREQVRLNRLAKVGGKVLRSAGVEPWYVRFVVEEGFARRVCGRESGRGDQECIDRV 886
Qy 631 NMYSSFYMAR 641
Db 887 NMYASCWILEK 897

RESULT 4

US-10-118-495-3

; Sequence 3, Application US/10118495

; Publication No. US20030074688A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; CURRENT APPLICATION NUMBER: US/10/118,495

; CURRENT FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: 60/283,812

; PRIOR FILING DATE: 2001-04-13

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Rhodobacter sphaeroides

US-10-118-495-3

Query Match 11.0%; Score 379.5; DB 4; Length 416;
Best Local Similarity 28.1%; Pred. No. 8.3e-29;
Matches 127; Conservative 68; Mismatches 182; Indels 75; Gaps 20;

Qy 231 TQGSIPYVWLRAPYVWIGRLPSVGHALH-----EERVERPMPPTF---LYTQSW 280
Db 2 TQFALTHLP---APP---VAR--QIGAAVHRTSLLSAEGLMER--MFSRLFHGLVYPOIW 51
Qy 281 EDPEPDMVMEINPKDVTTLTSGGCNALLVQAGQVSVDCNPAQSALLEKKVAIQ 340
Db 52 EDPVDMAAALAIRPGDRLVAITASGCGNVLSVLTQPGSILAVDLSPAVALGRKLAAAR 111
Qy 341 QL-BFEDVWOLFQEGVHPRIEELYEKKLAPFLSQTSHNFW-----SKRLWYFQHGLYYQ 393
Db 112 TLPDHAFFDLFGRADLPFGNAAALYDRHIAPALDGRSRYWEARSPFGRRIQLFERGFYRH 171
Qy 394 GGMKGLCWVLOCLAVVLGLGKTVKRLANAPTMEQRRLWDSNMLHFVKNVGNPKPLVWLFV 453
Db 172 GALGRFICAAHTLA--RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217
Qy 454 KFSVLVLNKAFLWFGGVPGKQVALIKADG---IPIENYIARTMDGVAENSH----- 503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGVLPV-----LRORLHRLLCDF 267
Qy 504 VRKONYFYNYNCLTGKFLRDN---CPTYLRREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVQIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGIVIVR---SASLSPPYAEILQKAGF 614
Db 112 TLPDHAFFDLFGRADLPFGNAAALYDRHIAPALDGRSRYWEARSPFGRRIQLFERGFYRH 171
Qy 394 GGMKGLCWVLOCLAVVLGLGKTVKRLANAPTMEQRRLWDSNMLHFVKNVGNPKPLVWLFV 453
Db 172 GALGRFICAAHTLA--RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217

Qy 454 KFSVLVLNKAFLWFGGVPGKQVALIKADG---IPIENYIARTMDGVAENSH----- 503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGVLPV-----LRORLHRLLCDF 267
Qy 504 VRKONYFYNYNCLTGKFLRDN---CPTYLRREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVQIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGIVIVR---SASLSPPYAEILQKAGF 614
Db 327 ESIHGFTLLDAQDQWMTDAQLTALNRQVTRTAAPGARVIFRTGGAADLLP--GRVPEEILG 384
Qy 615 DVCIRRTAQG--YMDRVNMYSSFYMAR 644
Db 385 HWRADRAAQAGHAADRSATYGGFHLRYRRDA 416

RESULT 5

US-10-620-914-3

; Sequence 3, Application US/10620914

; Publication No. US20040093639A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; FILE REFERENCE: MSU-07769

; CURRENT APPLICATION NUMBER: US/10/620,914

; CURRENT FILING DATE: 2003-07-16

; PRIOR APPLICATION NUMBER: 10/118,495

; PRIOR FILING DATE: 2002-04-08

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Rhodobacter sphaeroides

US-10-620-914-3

Query Match 11.0%; Score 379.5; DB 4; Length 416;
Best Local Similarity 28.1%; Pred. No. 8.3e-29;
Matches 127; Conservative 68; Mismatches 182; Indels 75; Gaps 20;

Qy 231 TQGSIPYVWLRAPYVWIGRLPSVGHALH-----EERVERPMPPTF---LYTQSW 280
Db 2 TQFALTHLP---APP---VAR--QIGAAVHRTSLLSAEGLMER--MFSRLFHGLVYPOIW 51
Qy 281 EDPEPDMVMEINPKDVTTLTSGGCNALLVQAGQVSVDCNPAQSALLEKKVAIQ 340
Db 52 EDPVDMAAALAIRPGDRLVAITASGCGNVLSVLTQPGSILAVDLSPAVALGRKLAAAR 111
Qy 341 QL-BFEDVWOLFQEGVHPRIEELYEKKLAPFLSQTSHNFW-----SKRLWYFQHGLYYQ 393
Db 112 TLPDHAFFDLFGRADLPFGNAAALYDRHIAPALDGRSRYWEARSPFGRRIQLFERGFYRH 171
Qy 394 GGMKGLCWVLOCLAVVLGLGKTVKRLANAPTMEQRRLWDSNMLHFVKNVGNPKPLVWLFV 453
Db 172 GALGRFICAAHTLA--RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217
Qy 454 KFSVLVLNKAFLWFGGVPGKQVALIKADG---IPIENYIARTMDGVAENSH----- 503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGVLPV-----LRORLHRLLCDF 267
Qy 504 VRKONYFYNYNCLTGKFLRDN---CPTYLRREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVQIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGIVIVR---SASLSPPYAEILQKAGF 614
Db 327 ESIHGFTLLDAQDQWMTDAQLTALNRQVTRTAAPGARVIFRTGGAADLLP--GRVPEEILG 384
Qy 615 DVCIRRTAQG--YMDRVNMYSSFYMAR 644

```

Db 385 HWRADRAAGAGHAADRSIAIYGGFHLXRRDA 416

RESULT 6
US-10-118-495-29
; Sequence 29, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-118-495-29

Query Match 9.4%; Score 326.5; DB 4; Length 416;
Best Local Similarity 27.8%; Pred. No. 1.9e-23;
Matches 111; Conservative 69; Mismatches 158; Indels 61; Gaps 16;

QY 275 LYTSQWEDPEPDMEVMEINPKDVTLTSTGGCNALNLLVQAGQVSVDCNPAQSALLEL 334
DB 44 VYQIWEDEPDMEAMELGEHGRIVTIGSGCNMLAYLSRNPASIDVDVLPHPHIALNKL 103
QY 335 KKVAIQOL-EPEDVWQLFGEVHPRIEELYEKKLAPFLSQTSHNFWK-----RLWYF 386
DB 104 KLAAPRHLPAHQDVVRHFGRAGRTRNSVGYDFIAEHLDAITTKAYWSKRTLSGRRRISVF 163
QY 387 QHGLYYQGGMGKLCWVLOCLAVLGLKTVKRLANAPTEBQRRLWDSNMLIHVFKNPK 446
DB 164 DRNIYRTGLLGRFTGAGHIMARLHGVLKLT--EMAKTRTLDQROFFDSKVAPLF---DK 217
QY 447 PLV-WLFVKFVSLVLFNKAVLWFGGVPKGQY---ALIKADGIPYENIARTMDGVAENS 502
DB 218 PVVRLWTKRKSLL-----FGLGIPPRQYDELASLSSDG-TVASVLKERLEKLAACNF 267
QY 503 HVRKQNYFYNCLTGKFLRDN---CPTYLRBAAPATLKSQVVDNLTVSTNFFMEELK--- 556
DB 268 PL-SDNYFAWQAFARRYPEPEHGAIPAYLKPEYKIRNNTA-RVAVHHATYTELLSRKP 325
QY 557 ARTYKVLMDHVDWLDMPVANELAECLAQVAPGGIVWRSAS-----LSPPYAEL 608
DB 326 ANGVDRIYLLDAQDMWTDVQLNELWSQISRTAASGARVIFRTAAEKSVEIGRLSP----- 380

QY 609 IQKAGFDVR-----CIRRATO-GYMDRVNMYSSFFYMARR 641
DB 381 -----DIRNQWVLEERSNELNAMDRSIAIYGGFHIYOR 413

RESULT 7
US-10-620-914-29
; Sequence 29, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52

```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-620-914-29

Query Match 9.4%; Score 326.5; DB 4; Length 416;
Best Local Similarity 27.8%; Pred. No. 1.9e-23;
Matches 111; Conservative 69; Mismatches 158; Indels 61; Gaps 16;

QY 275 LYTSQWEDPEPDMEVMEINPKDVTLTSTGGCNALNLLVQAGQVSVDCNPAQSALLEL 334
DB 44 VYQIWEDEPDMEAMELGEHGRIVTIGSGCNMLAYLSRNPASIDVDVLPHPHIALNKL 103
QY 335 KKVAIQOL-EPEDVWQLFGEVHPRIEELYEKKLAPFLSQTSHNFWK-----RLWYF 386
DB 104 KLAAPRHLPAHQDVVRHFGRAGRTRNSVGYDFIAEHLDAITTKAYWSKRTLSGRRRISVF 163
QY 387 QHGLYYQGGMGKLCWVLOCLAVLGLKTVKRLANAPTEBQRRLWDSNMLIHVFKNPK 446
DB 164 DRNIYRTGLLGRFTGAGHIMARLHGVLKLT--EMAKTRTLDQROFFDSKVAPLF---DK 217
QY 447 PLV-WLFVKFVSLVLFNKAVLWFGGVPKGQY---ALIKADGIPYENIARTMDGVAENS 502
DB 218 PVVRLWTKRKSLL-----FGLGIPPRQYDELASLSSDG-TVASVLKERLEKLAACNF 267
QY 503 HVRKQNYFYNCLTGKFLRDN---CPTYLRBAAPATLKSQVVDNLTVSTNFFMEELK--- 556
DB 268 PL-SDNYFAWQAFARRYPEPEHGAIPAYLKPEYKIRNNTA-RVAVHHATYTELLSRKP 325
QY 557 ARTYKVLMDHVDWLDMPVANELAECLAQVAPGGIVWRSAS-----LSPPYAEL 608
DB 326 ANGVDRIYLLDAQDMWTDVQLNELWSQISRTAASGARVIFRTAAEKSVEIGRLSP----- 380

QY 609 IQKAGFDVR-----CIRRATO-GYMDRVNMYSSFFYMARR 641
DB 381 -----DIRNQWVLEERSNELNAMDRSIAIYGGFHIYOR 413

RESULT 8
US-10-118-495-41
; Sequence 41, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-118-495-41

Query Match 9.3%; Score 321; DB 4; Length 415;
Best Local Similarity 26.2%; Pred. No. 6.7e-23;
Matches 113; Conservative 70; Mismatches 176; Indels 72; Gaps 18;

QY 255 VGHALHEERV-----ERPPMFPPTF---LYTSQWEDPEPDMEVMEINPKDVTLTSG 304
DB 16 VGVAVYQNRALSQAGISER--LFAPLFGSLVYVYQIWEDEPDVDMQVQGHRIVTIASG 73
QY 305 GCNALNLLVQAGQVSVDCNPAQSALLELKKVAIQOLEFE-DVWQLFGEVHPRIEELY 363
DB 74 GCNLIAYLTRSPARIDAVDLNAAHIALNRMLKLEAVRRLPSQGDLPFRFFGAADTSHNSQAY 133

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Qy 364 EKXAPFISQTSNFWSKRLM-----YFOHGLYYQGMGKLCWVLOCLAVVLG----- 411
 Db 134 DRFIAPHLDPVSRHYWERRNRGRRRIAVFORNFYQTGLLG-----LFIAMGHRTAK 185
 Qy 412 -LGKTVKRLANAPTMEQORLWDSNMLIHFVKNGPKPLVWLFVKFVSLVFNKAVLWFGG 470
 Db 186 FFGVNPAMMEARNIGEORRFNEELAPVFDK---KLLKWATSRKASL-----FGL 233
 Qy 471 GVPQKQY--ALIKADGIPNIYIAR---TMDGVAENSHVRKQNYFYNYCLTGTFLRDN- 523
 Db 234 GIPPAQYDSLITSGDGTWASVLKARLEKACDFPLEN-----NYFAWQAFARVPNPE 287
 Qy 524 --CPTYLREAAATLKSGVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMPVAN 578
 Db 288 AALPAYLEKQNYETIR-GNIDRVVAIHANLIEFLAGKDAGTVDRFILLDAQDMMTDDQLN 346
 Qy 579 ELAECLAQKQVAPGGIVWIRSA---SLSP--PYAELIQKAGFVRCIRATQGYMDRVNMY 633
 Db 347 ALMSEISRTASAGARVIFRTAAEPSLLPGRVSTSLDDQWDYQDEASREFSA--RDRSAIY 404
 Qy 634 SSFYMARKGA 644
 Db 405 GGFHLYVKRTA 415

RESULT 9
 US-10-620-914-41
 ; Sequence 41, Application US/10620914
 ; Publication No. US20040093639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph
 ; APPLICANT: Riekhof, Wayne
 ; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-07769
 ; CURRENT APPLICATION NUMBER: US/10/620,914
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 10/118,495
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 41
 ; LENGTH: 415
 ; TYPE: PRT
 ; ORGANISM: Mesorhizobium loti
 US-10-620-914-41

Query Match 9.3%; Score 321; DB 4; Length 415;
 Best Local Similarity 26.2%; Pred. No. 6.7e-23;
 Matches 113; Conservative 70; Mismatches 176; Indels 72; Gaps 16;
 Qy 255 VGHALHEERV-----ERPMPFPTF---LYTOSWEDPEPDMVMEINPKDVTLTLSG 304
 Db 16 VGKAVYQNRALSAGISER--LFAFLFSLGVLTPQIWEPPDVMQGLGQGHRIVTIASG 73
 Qy 305 GCNALNLIVQAGQVSDVCNPAQSALLEKKVAIQLEFE-DVMQLFGEGVHPRIEBLY 363
 Db 74 GCNLAIVLTRSPARIDAVDNAIALNRMKLEAVRPLPSQGLDFRFFGAADTSHNSQAY 133
 Qy 364 EKXAPFISQTSNFWSKRLM-----YFOHGLYYQGMGKLCWVLOCLAVVLG----- 411
 Db 134 DRFIAPHLDPVSRHYWERRNRGRRRIAVFORNFYQTGLLG-----LFIAMGHRTAK 185
 Qy 412 -LGKTVKRLANAPTMEQORLWDSNMLIHFVKNGPKPLVWLFVKFVSLVFNKAVLWFGG 470
 Db 186 FFGVNPAMMEARNIGEORRFNEELAPVFDK---KLLKWATSRKASL-----FGL 233
 Qy 471 GVPQKQY--ALIKADGIPNIYIAR---TMDGVAENSHVRKQNYFYNYCLTGTFLRDN- 523
 Db 234 GIPPAQYDSLITSGDGTWASVLKARLEKACDFPLEN-----NYFAWQAFARVPNPE 287
 Qy 524 --CPTYLREAAATLKSGVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMPVAN 578

Db 288 AALPAYLEKQNYETIR-GNIDRVVAIHANLIEFLAGKDAGTVDRFILLDAQDMMTDDQLN 346
 Qy 579 ELAECLAQKQVAPGGIVWIRSA---SLSP--PYAELIQKAGFVRCIRATQGYMDRVNMY 633
 Db 347 ALMSEISRTASAGARVIFRTAAEPSLLPGRVSTSLDDQWDYQDEASREFSA--RDRSAIY 404
 Qy 634 SSFYMARKGA 644
 Db 405 GGFHLYVKRTA 415

RESULT 10
 US-10-118-495-33
 ; Sequence 33, Application US/10118495
 ; Publication No. US20030074688A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph
 ; APPLICANT: Riekhof, Wayne
 ; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-06897
 ; CURRENT APPLICATION NUMBER: US/10/118,495
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: 60/283,812
 ; PRIOR FILING DATE: 2001-04-13
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 416
 ; TYPE: PRT
 ; ORGANISM: Sinorhizobium meliloti
 US-10-118-495-33

Query Match 8.4%; Score 292.5; DB 4; Length 416;
 Best Local Similarity 26.0%; Pred. No. 5.1e-20;
 Matches 102; Conservative 71; Mismatches 174; Indels 45; Gaps 16;
 Qy 275 LYTOSWEDPEPDMVMEINPKDVTLTLSGDCNALNLIVQAGQVSDVCNPAQSALLEL 334
 Db 45 VYQIWEPPDVMQGLGQGHRIVTIGSGGCNMLTVLSAEPARIDVVDLNPHTALNRL 104
 Qy 335 KKVAIQQL-EFEDVWQLFG-BGVHPRIEBLYEKKLAPLSQTSNFWFS-----KRLWY 385
 Db 105 KLSAFRHLPSHKDYVREFLAVEGTRTN-GQAYDVFLAPKLDPATRAYMNGRDLTGRRRIGV 163
 Qy 386 FQHGLYYQGMGKLCWVLOCLAVVLGKTVKRLANAPTMEQORLWDSNMLIHFVKNGP 445
 Db 164 FGRNVYTGLLGRFISASHALARLHGINP--EDPVKARSMREQQFFDDKLAFLP----E 217
 Qy 446 KPLV-WLFFVKFVSLVFNKAVLWFGGVGVPDKQYALIKADGIPNIYIARTMDGVAENSHV 504
 Db 218 RPVIRWITSRSSL-----FGLGIPPOQFDELAS--LSREKSVAAVLNRLEKLTLC 266
 Qy 505 R---KQNYFYNYCLTGTFLRDN---CPTYLREAAATLKSGVDNLTVSTNFFMEEL--- 555
 Db 267 HFPLRDNVYFAWQAFARVPNPEDEGELPPYLOQASRYEARIDN-ABRVEVHHASFTELLAGK 325
 Qy 556 KARTYTKVILMDHVDWLDMPVANLEAELAKQVAPGGIVWIRSA---ASLSP--YAEILIQ 610
 Db 326 PAASVDRIVLDDAQDMMTDDQLNDLWTEITKTADAGAVVIFRTAAEASILPRLSTTLDD 385
 Qy 611 KAGFVRCIRATQGYMDRVNMYSSFYMARK 642
 Db 386 QWYDAETSMRL--GAEDRSALYGGFHYRKK 415

RESULT 11
 US-10-620-914-33
 ; Sequence 33, Application US/10620914
 ; Publication No. US20040093639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph

```

; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 33
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-620-914-33

```

```

Query Match      8.4%; Score 292.5; DB 4; Length 416;
Best Local Similarity 26.0%; Pred. No. 5.1e-20;
Matches 102; Conservative 71; Mismatches 174; Indels 45; Gaps 16;

Qy 275 LYTSWEDPEPMEVMEINPKDVLTLTSGGCNALLVQAGQVSVDCNPAQSALLEL 334
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 45 VYQIWEPIVDMQAMQIRPGHRIVTIGSGGCNMLTYLSAEPARIDVVDLNPPIALNRL 104
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 335 KKVAIQOL-EPEDVWQFQ-EGVHPRIEELYEKKLAPLSQTSNFWG-----KRLWY 385
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 105 KLSAPRHLPSHKDVVRFAVEGTRTN-GQAYDVFLAPKLDPATRAYMNGRDLTGRRRIGV 163
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 386 FOHGLYQGGMGKLCWVLQCLAVLGLGKTKVRLANAPTMEEQRLWDSNNLIHFVNKGP 445
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 164 FGRNVYRTGLLGRFISASHALRHLGNP--EDFVKARSMEQRFDDKLAFLF---E 217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 446 KPLV-WLFVKFVSLVFNKAVLWFGGVPQKQYALIKADGPIENYIARTWDGVAENSHV 504
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 218 RPVIRWITSRKSLL-----FGLGIPPPQFDELAS--LSREKSAVAALNRLEKLT 266
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 505 R---KQNYFYNCITGKFLRDN---CPTYLEAFAATLKSGVDNLTVSTNFMEEEL--- 555
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 267 HFPLRDNFVWQAFRRYPRDEGELPPYLOASRYEARDN-AERVEVHHASFTELLGAK 325
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 556 KARTYTKVILMDHVDLMDPVANELAECLAKQVAPGGIVWRS---ASLSP--YAEILQ 610
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 326 PAASVDRVILDAQDMWTDQQLNDLWTEITRTADAGAVVIFRTAAEASILFGLSTLLD 385
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 611 KAGFDVRCIRATQGYMDRVNYSFYMARK 642
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 386 QWYDAETSMRL--GAEDRSIYGGFHIYRKK 415
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 12
US-10-684-141-58
; Sequence 58, Application US/10684141
; Publication No. US2005003536A1
; GENERAL INFORMATION:
; APPLICANT: Furusawa, Mitsuru
; TITLE OF INVENTION: METHOD AND SYSTEM FOR RAPIDLY CONFERRING
; FILE REFERENCE: 690116.401
; CURRENT APPLICATION NUMBER: US/10/684,141
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2284
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-684-141-58

Query Match      3.6%; Score 123; DB 5; Length 2284;
Best Local Similarity 20.8%; Pred. No. 0.094;
Matches 141; Conservative 79; Mismatches 217; Indels 240; Gaps 35;

Qy 107 HSLCEVAKKAKAK-GWKNVQVVEADACQAPPEGTATLITFSYS----- 150

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Db 422 HNL-----KAAAKAKLGYDPELDPEDMCRVA-TSQPTLATYSVSDAVATYLYMYKYP 476
Qy 151 -----LTMIPPH-NVI-----DQACYSLSQDGLVGA 177
Db 477 FIFALCTIIPMEPDEVLRKSGTLCCEALLMVQAFHANIIFPNKQEQEFNKLTDDGHVDA 536
Qy 178 DFYVSG-----KYDLP--LRQMPWSRRFFWRISFDIDNIDIGERRAYLEQ--KL 223
Db 537 ETVYGGHVEALESVGFRRSDIPCRFRMMPAAPDFLLQVKEKTRMRHAIEEEKVPVEQATNF 596
Qy 224 ERVMEQ--NTQGSIPYVWLRAPYVYVWIGRLPSVGHALHEERVERP-----PMFPPT 273
Db 597 QEVCEQIKTKLTSLKQVP-----NRIECPLIYHLDVDGAMYNI 634
Qy 274 FLYTSWEDPEPMEVMEINPKDVLTLTSGGCN-----ALNLLVQAGQVSVSDCN 325
Db 635 ILTNR-----LQPSAIVDEATCAACDFNFKPGASCORIMAWQWGEFM----- 676
Qy 326 PAQSALLELKKVAIQOLEFEDVWOLFEGGVHPRIEEL-----YEK-KLAPF----- 370
Db 677 PASRS--EYHRIQ-HQLESEKFPPLFPEGPARAFHLSREEQAKYEKRLADYCKKAYKK 733
Qy 371 -----LSQTSNFMWSKELWYFQHGYYQGGMGKLCWVLQCLAVLGLGKTVKR 418
Db 734 IHVTKVEERLTTICORENSFYVDTVRAFRRDRRYEFGHLHKVKKLSAAVEVGDASEVKR 793
Qy 419 LANAPTMBEQRLWDSNNLIH-----FVNGKPKLVWLFWKFSVLVFNKAVLWF 468
Db 794 CKN-----MEILYDSLQLAHKCILNSFYGYVMRKAR---WYSMEMAGIVCFT----- 838
Qy 469 GGGVPGQYALIKADGPI-----ENVIARTMDGVAENSHVRKQNYFY 512
Db 839 GANITQARELIEQIGRPLELDTDGIWCVLNSFPENFIKT-----TNAKKPKLTISYP 893
Qy 513 NCLAGKFLRDNCTPY---LREAAAFATLKSGVDNLTVSTNFMEEELKARTYTKVILMDH 568
Db 894 GAMLNIMVKEGFTNHQYQELTEPSSLTY-----VTHSENSIPEVDG-PYLAMIL--- 942
Qy 569 VDWLMDPVANELAECLAKQVAPGGIVWRSASLPPYAEILQKAGFDVRCIRATQGYMD 628
Db 943 -----PASKKEGKKLKKRYA---VFNEDGSL-----AEL---KGFEVK-----RRBELQ 980
Qy 629 RVNMY-SSFYMARKGA 644
Db 981 LIKIFQSVFEAFILKGS 997

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RESULT 13
US-10-810-486-58
; Sequence 58, Application US/10810486
; Publication No. US20050054597A1
; GENERAL INFORMATION:
; APPLICANT: Furusawa, Mitsuru
; TITLE OF INVENTION: METHOD AND SYSTEM FOR RAPIDLY CONFERRING
; FILE REFERENCE: 690116.401C1
; CURRENT APPLICATION NUMBER: US/10/810,486
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/684,141
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: JP 2003-092898
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 58
; LENGTH: 2284
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-810-486-58

Query Match      3.6%; Score 123; DB 5; Length 2284;
Best Local Similarity 20.8%; Pred. No. 0.094;

```

```

Matches 141; Conservative 79; Mismatches 217; Indels 240; Gaps 35;
QY 107 HSLCEVAKKAKAK-GWRNVQVVEADACQAPPEGTATLITFSY- 150
Db 422 HNL-----KAAKAKLGYDVELDPEDMCRMA-TEQPQTATYSVSDAVATYYLYKYYHP 476
QY 151 -----LTMPPFH-NVI-----DQACSYLSQDGLVGVA 177
Db 477 FIFALCTIIPPEPDLVRKSGTLCALLMQAFHANIIFPNKQBEFNKLTDDGHVLDA 536
QY 178 DFYVSG-----KYDLP--LRMPWSRRFFWRSIFDINDIDIGPERRAYLEQ--KL 223
Db 537 ETVVGGHVEALESYGFRSDIPCRFRMNPAADFLLORVEKTKWHAIEEEKVPVQATNF 596
QY 224 ERVWEQ--NTQGSIPYVWMLRAPYYVWIGRLPSVGHALHEERVERP-----PMFPPT 273
Db 597 QEVCEQIKTKLTKDVP-----NRIECPLIYHLDVGAMYENI 634
QY 274 FLYTQSWEDPEDMEVMEINPKDVTILTSGCCN-----ALNLLVQGGQVVSVDN 325
Db 635 ILTWR-----LQPSAIVDEATCAACDFNKGASCQKQKMAQWGRGEM----- 676
QY 326 PAQSALLEKKAIVAIQOLFEDVWOLFGRGVHPRIEEL-----YEK-KLAPP----- 370
Db 677 PASRS--BYHRIQ-HOLESEKFPPLFPEGAPAFHLSREBOAKYKRRRLADYCKKAYKK 733
QY 371 -----LSQTSNFWKRLWYFQHGGLYQGGMGKLCWLQCLAVVLGLGKTYYR 418
Db 734 IHVTKVEERLITICQRENSFYVDTVRAFDRDRYEFKGLHWKVKKLSAAVEVGDASEVKR 793
QY 419 LANAPTMEQRRLDNSNLIH-----FVKNPKPLVWLFWKFSVLVLFNKAVLWF 468
Db 794 CKN-----MEILDVSLQLAHKCILNSFYGYMKRGAR--WYSMEMAGIVCFT----- 838
QY 469 GGGVPGKQYALIKADGIPI-----ENVIARTMDGVAENSHVRKQNYFY 512
Db 839 GANITQARELIEQIGREPLEDTGICWVLPNSPFENFVIKT-----TNKKPKLTISYP 893
QY 513 NCLTGKFLRDNCTY-----LREAAFPATLKSGVDNLTVSTNFFMBELKARTYTYKVLMDH 568
Db 894 GAMLNIMVKEGFTNHQYQELTEPSSLTY-----VTHSENSIPEVDG-PYLAMIL--- 942
QY 569 VDWMMPVANLAECLAKQVAPGGIVWRSASLSPPYAELIQKAGFDVRCIRRTAQGYMD 628
Db 943 -----PASKEEGKLLKRYA---VFNEDGSL-----AEL---KGFEVK-----RRGELQ 980
QY 629 RVNMY-SSFYMARKGA 644
Db 981 LIKIFQSSVFEAFUKGS 997

RESULT 14
US-10-118-495-35
; Sequence 35, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-35

Matches 141; Conservative 79; Mismatches 217; Indels 240; Gaps 35;
QY 107 HSLCEVAKKAKAK-GWRNVQVVEADACQAPPEGTATLITFSY- 150
Db 422 HNL-----KAAKAKLGYDVELDPEDMCRMA-TEQPQTATYSVSDAVATYYLYKYYHP 476
QY 151 -----LTMPPFH-NVI-----DQACSYLSQDGLVGVA 177
Db 477 FIFALCTIIPPEPDLVRKSGTLCALLMQAFHANIIFPNKQBEFNKLTDDGHVLDA 536
QY 178 DFYVSG-----KYDLP--LRMPWSRRFFWRSIFDINDIDIGPERRAYLEQ--KL 223
Db 537 ETVVGGHVEALESYGFRSDIPCRFRMNPAADFLLORVEKTKWHAIEEEKVPVQATNF 596
QY 224 ERVWEQ--NTQGSIPYVWMLRAPYYVWIGRLPSVGHALHEERVERP-----PMFPPT 273
Db 597 QEVCEQIKTKLTKDVP-----NRIECPLIYHLDVGAMYENI 634
QY 274 FLYTQSWEDPEDMEVMEINPKDVTILTSGCCN-----ALNLLVQGGQVVSVDN 325
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QY 326 PAQSALLEKKAIVAIQOLFEDVWOLFGRGVHPRIEEL-----YEK-KLAPP----- 370
Db 677 PASRS--BYHRIQ-HOLESEKFPPLFPEGAPAFHLSREBOAKYKRRRLADYCKKAYKK 733
QY 371 -----LSQTSNFWKRLWYFQHGGLYQGGMGKLCWLQCLAVVLGLGKTYYR 418
Db 734 IHVTKVEERLITICQRENSFYVDTVRAFDRDRYEFKGLHWKVKKLSAAVEVGDASEVKR 793
QY 419 LANAPTMEQRRLDNSNLIH-----FVKNPKPLVWLFWKFSVLVLFNKAVLWF 468
Db 794 CKN-----MEILDVSLQLAHKCILNSFYGYMKRGAR--WYSMEMAGIVCFT----- 838
QY 469 GGGVPGKQYALIKADGIPI-----ENVIARTMDGVAENSHVRKQNYFY 512
Db 839 GANITQARELIEQIGREPLEDTGICWVLPNSPFENFVIKT-----TNKKPKLTISYP 893
QY 513 NCLTGKFLRDNCTY-----LREAAFPATLKSGVDNLTVSTNFFMBELKARTYTYKVLMDH 568
Db 894 GAMLNIMVKEGFTNHQYQELTEPSSLTY-----VTHSENSIPEVDG-PYLAMIL--- 942
QY 569 VDWMMPVANLAECLAKQVAPGGIVWRSASLSPPYAELIQKAGFDVRCIRRTAQGYMD 628
Db 943 -----PASKEEGKLLKRYA---VFNEDGSL-----AEL---KGFEVK-----RRGELQ 980
QY 629 RVNMY-SSFYMARKGA 644
Db 981 LIKIFQSSVFEAFUKGS 997

RESULT 14
US-10-118-495-35
; Sequence 35, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-35

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Query Match 3.5%; Score 120; DB 4; Length 221;
Best Local Similarity 24.1%; Pred. No. 0.0051;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 6;
QY 75 VDLGGGTGENDMADYIDLAKFKSIYVVDLCHLSLCEVAKKAKAKGKWNQVQVVEADACQ 134
Db 53 LEVGGGTGRNLAVIGDLYPGAR---LFGLDISAEMLATAKAKLRRQNRPDVLRVADATN 109
QY 135 FA----PPEGTATLITFSYSLTMIPTPHNVIDQACSYLSQDGLVGADFYVSGKYDLP 190
Db 110 FTAASFQOEGFDRIV-ISYALSMVPEWEKAVDAATAALKPGGSLHIADFGQOEGWPAGFR 168
QY 191 Q--MPWSRRFF---WRSIFDIDN-----IDIGPERRAY 218
Db 169 RFLQAWLRRFHVTPRETILFDVMKRAERNDAALAEVRSLSRGY 210

RESULT 15
US-10-620-914-35
; Sequence 35, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; PRIOR FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-620-914-35

Query Match 3.5%; Score 120; DB 4; Length 221;
Best Local Similarity 24.1%; Pred. No. 0.0051;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 6;
QY 75 VDLGGGTGENDMADYIDLAKFKSIYVVDLCHLSLCEVAKKAKAKGKWNQVQVVEADACQ 134
Db 53 LEVGGGTGRNLAVIGDLYPGAR---LFGLDISAEMLATAKAKLRRQNRPDVLRVADATN 109
QY 135 FA----PPEGTATLITFSYSLTMIPTPHNVIDQACSYLSQDGLVGADFYVSGKYDLP 190
Db 110 FTAASFQOEGFDRIV-ISYALSMVPEWEKAVDAATAALKPGGSLHIADFGQOEGWPAGFR 168
QY 191 Q--MPWSRRFF---WRSIFDIDN-----IDIGPERRAY 218
Db 169 RFLQAWLRRFHVTPRETILFDVMKRAERNDAALAEVRSLSRGY 210

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)
652.011 Million cell updates/sec

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Perfect score: 3463
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:*
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2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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6: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	3.1	472	11	US-11-169-041-156
2	106	3.1	684	11	US-11-079-463-7496
3	102	2.9	448	11	US-11-124-367A-282
4	101.5	2.9	865	11	US-11-079-463-9886
5	101	2.9	688	11	US-11-079-463-7941
6	99	2.9	549	11	US-11-188-298-13759
7	97	2.8	2209	10	US-11-301-554-1903
8	96	2.8	326	9	US-10-467-657-7224
9	95.5	2.8	2890	11	US-11-115-639-31
10	95.5	2.8	2890	11	US-11-115-639-32
11	95.5	2.8	2890	11	US-11-115-639-33
12	94	2.7	658	11	US-11-096-568A-2582
13	94	2.7	660	11	US-11-096-568A-2581
14	94	2.7	680	11	US-11-096-568A-2580
15	93.5	2.7	344	11	US-11-153-185-7
16	93.5	2.7	1197	9	US-10-055-877-8
17	93.5	2.7	1247	9	US-10-055-877-10
18	93	2.7	417	11	US-11-098-686-11330
19	92.5	2.7	358	11	US-11-045-004-2727
20	92.5	2.7	1590	9	US-10-055-877-146
21	92	2.7	316	11	US-11-096-568A-1265

22	92	2.7	477	11	US-11-079-463-9020	Sequence 9020, Ap
23	91.5	2.6	241	11	US-11-098-686-10262	Sequence 10262, A
24	91.5	2.6	389	11	US-11-079-463-8258	Sequence 8258, Ap
25	91	2.6	749	11	US-11-072-512-2622	Sequence 2622, Ap
26	90.5	2.6	1249	9	US-10-506-454-486	Sequence 486, App
27	89	2.6	537	11	US-11-109-156-28	Sequence 28, Appl
28	89	2.6	577	9	US-10-718-264-3	Sequence 3, Appl
29	89	2.6	577	9	US-10-718-264-3	Sequence 3, Appl
30	89	2.6	577	11	US-11-176-667-3	Sequence 3, Appl
31	88.5	2.6	329	11	US-11-234-786-376	Sequence 376, App
32	88.5	2.6	329	11	US-11-139-041-299	Sequence 299, App
33	88	2.5	217	11	US-11-188-298-9904	Sequence 9904, Ap
34	87.5	2.5	237	11	US-11-045-004-1923	Sequence 1923, Ap
35	87.5	2.5	834	11	US-11-087-099-10005	Sequence 10005, A
36	87.5	2.5	852	11	US-11-188-298-14739	Sequence 14739, A
37	87	2.5	243	11	US-11-153-185-4	Sequence 4, Appl
38	87	2.5	265	9	US-10-467-657-6590	Sequence 6590, Ap
39	87	2.5	265	9	US-10-467-657-7654	Sequence 7654, Ap
40	87	2.5	335	11	US-11-153-185-3	Sequence 3, Appl
41	87	2.5	338	11	US-11-153-185-5	Sequence 5, Appl
42	87	2.5	339	11	US-11-153-185-2	Sequence 2, Appl
43	87	2.5	565	11	US-11-072-512-2180	Sequence 2180, Ap
44	86.5	2.5	395	9	US-10-793-626-664	Sequence 664, App
45	86.5	2.5	431	9	US-10-506-454-1573	Sequence 1573, Ap

ALIGNMENTS

RESULT 1
US-11-169-041-156
; Sequence 156, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; PRIOR FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-156

Query Match 3.1%; Score 106; DB 11; Length 472;
Best Local Similarity 20.4%; Pred. No. 0.22;
Matches 90; Conservative 54; Mismatches 155; Indels 142; Gaps 19;

QY	12	YTKNFSLEKILKLSMKDDLTVLRLHMFSGSKGGDDHAA-----RLSEFYGPOAA--AFAA 64
DB	39	FYRTEFQNRFEK-ATMNCNLLAYLXHL-----KQNEAALECLRKAEELIQEHADQAEIR 92
QY	65	RLAERSNLIWDLGGGTGENVDMADYID--LAKFKSIYVVDLCHSLCEVAKKKAKAGW 122
DB	93	SLVTWGNVAYYYHMGRLSDVQIYVDKVKHVCESFSPYRIESPELDCBEGWTRLKCGN 152
QY	123	KN--VOVVEADACQFAP--PEGTATLITFSYSLTWIPPHNVIDQACSVLSQDLGVGVAD 178
DB	153	QNERAKVCFEALBKPKNPEFTSGLTAASRLONWPPSQNAID----- 196
QY	179	FVYSGKYDLPLRQMPWSRRFFWRSTFIDINDIDIGPER---RAYLEQKLERVWEQNTQGS 235
DB	197	-----PLRQA-----IRLNPDNQYLKVLALKLHKMREE----- 225
QY	236	PYPWMLRAPYYWIGRLPSVGHALHEERVRPP-----MFPPTFLYTQSWEDPEDNEV-- 289

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Db 226 -----GEEGEGEKLVEALEKAPGVTVDVLSAAKPYRRKDEPDKAIELK 271
Qy 290 --MBINPKDVTLTITSGGCNALLVQAGQVVSVDNCP--AQSALELKKVAIQOL--- 342
Db 272 KALEYIPNNAYLHCQIGCCYRAKVF-----QVMNLRENGMYGKRKLELIGHAVALHKA 326
Qy 343 -----EPEDWQLFGEGVHPRIEBELYEKKLAPFLSQTSH----- 376
Db 327 DEANDNLFRVCSILASLHALADQVEDABYF-----QKEFSKELTPVAKQLLHLRYG 378
Qy 377 NFW-----SKRLWYFOHGL 390
Db 379 NFQLYQMKCEDKAIHHFIEGV 399

RESULT 2
US-11-079-463-7496
; Sequence 7496, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7496
; LENGTH: 684
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-7496

Query Match 3.1%; Score 106; DB 11; Length 684;
Best Local Similarity 20.1%; Pred. No. 0.38;
Matches 120; Conservative 70; Mismatches 218; Indels 188; Gaps 30;

Qy 127 VVEADACQFAPPEGATLITFSYSLTM-----IppPHNVI---DOACS YLSODGL 173
Db 13 VILLTACGAKKNTAEADNFYVQEQADIQLRYRVPGFENLTLOKELVYILTQAL 72
Qy 174 VGVAD--FYVSGKYDLPLRQMPWSRRFFWRSIFDIDNIDIGPERRAYLEQKLEWQON- 230
Db 73 EG-RDILFDQNGKYNLTIRM-----LETIYDTYTGDRNSPDVNLTTYLKRVWFSNG 124
Qy 231 ---TQGSIPYVWL-----RAPYYVWIGRLPSVGHALHEEVER--PPMPPPTFL----- 275
Db 125 IHHYGESEKFPVGFTEFLKQALLSVDASKPLAQOGTVQQLFEELSVPVIFDPKVPKRV 184
Qy 276 -----YTQSWDEPEPMWEI-----NPKDVTLTITSGGCNALLVQAGQV 319
Db 185 NQAGEDLVLTASNYDGVTOQEAFAFNALKNPKDE--TPVSGLN--SRLVKEDCKI 240
Qy 320 VSDCNPAQSALLELKKVAIQOLEFEDVWQLFGEGVHPRIEBELYEKKLAPFLSQTSHFW 379
Db 241 I-----EKWKVGG-----LYTQAIKIV-----YV 261
Qy 380 SKRLWYFOHGLYQGGMGKLCWVLOCLAVVLGLKTVK--RLANAPTMBEQRLW--DSN 435
Db 262 LKKA-----EG-----VAEDDAQKAIGKLIBEYETGDLKTFDEYAILMVKDLN 305
Qy 436 MLIHFVKN-----GPKPLWLVFVKVSL-----VLFNKAVLWFGGVP--CKQVAL 479
Db 306 SRVFTNGFTSYGDPGLGKASWESIVNFKDLEARTRELTISSNAQWFDHSPVDKQFKK 365
Qy 480 IKADGIPIENYARTMDGVAENSHVRKQNYFYNNCLTGKFLRDNCPYTLREAAFATLKS 539
Db 366 EKVKGVTAKVITAAITLG-----DLYPSTAIGINLPNSNWIIRSHGS-----KSV 410
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Qy 540 VVDNLT-----VSTNPFMEELKARTYTKVILMDHVDMLDMPVANELAECL---AKOVAP 590
Db 411 TIGNITDAYNKAHNGFNBEFVYSDTEKQIDIKYAD--LTGELHTDHLHECLHGSGKLLP 469
Qy 591 GGIWIRSASLSP-----PYABELIQAGFDPVRCIRRATQGYMDRVNMYSSFYMARRK 642
Db 470 G-----VDPDALKAYGSTIEA-----RADLFLGYIVVADPK 500

RESULT 3
US-11-124-367A-282
; Sequence 282, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-282

Query Match 2.9%; Score 102; DB 11; Length 448;
Best Local Similarity 20.8%; Pred. No. 0.47;
Matches 90; Conservative 54; Mismatches 163; Indels 126; Gaps 19;

Qy 12 YTKNFSLEKLIKLSMKDDLTVLARMWFGSKGGDHAA-----RLESFYGPOAA--AFAA 64
Db 15 FYRTEFQNRPEK-ATMNCNLLAYLAKHL-----KGQNEAALECLRKAEELIQEHADQAEIR 68
Qy 65 PLAERSNLIWDLGGGTGCVNMDMADYID--LAKFKSYVVDLCHSLCEVAKKAKAGW 122
Db 69 SLVTWGNAYVYVYHNGRLSDVQIYVDKVKHCEKFSFYRIESPELDCBEGWTRLUKCGN 128
Qy 123 KN--VQVVEADACQFAP--PEGTATLITFSYSLTMIPPFHNVIDQACS YLSQDGLGVAD 178
Db 129 QNERAKVCFEKALEKKPKNPEFTSGLAISYRLDNWPPSQNAID----- 172
Qy 179 FYVSGKYDLPLRQMPWSRRFFWRSIFDIDNIDIGPER--RAYLEQKLEWQONTOQSI 235
Db 173 -----PLRQA-----IRLNPDNQYLKVLALKLHMKREE----- 201
Qy 236 PYVPLRPYVWVIGRLPSVGHALHEEVERPP-----MFPPTFLYQSWEDPEPMWEV-- 289
Db 202 -----GEEGEGEKLVEALEKAPGVTVDVLSAAKPYRRKDEPDKAIELK 247
Qy 290 --MEINPKDVTLTITSGGCNALLVQAGQVVSVDNCP--AQSALELKKVAIQOLEFE 345
Db 248 KALEYIPNNAYLHCQIGCCYRAKVF-----QVMNLRENGMYGKRKLELIGHAVALHKA 302
Qy 346 D-----VWQLFG-----EGVHPRIEBELYEKKLAPFLSQTSH-----NFW----- 379
Db 303 DEANDNLFRVCSILASLHALADQVEABEYFQKEFSKELTPVAKQLLHLRYGNFOLYOMK 362
Qy 380 --SKELWYFOHGL 390
Db 363 CEDKAIHHFIEGV 375
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Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 103; Conservative 66; Mismatches 177; Indels 170; Gaps 25;

Qy 207 DNIDIGERRAYLEOKL---ERVWEQNTQG--SIPYVPWLRAPYYVWIGRLPSVGHALHE 261
Db 58 DEIBIFESKPLTNLMLAMSEKIREQFRAGLESSP-----INMLPSYNHAL-- 103
Qy 262 ERVERPMPFPFTLYTQSWEDPEPDMVMEINPKDVTILTSTGCGN---ALNLLVOGAG 317
Db 104 -----PTG-----EGTFLALDVGGSTWRVALIELCGGOKM 135
Qy 318 QVSVDCNPAQSALLEKKVAIQOLEFEDVMQLFEGVHPRIEEL---YEKKLAPF----- 370
Db 136 EVLRV-----SSSLJDNDVKLLECTSFFD-W--MAEKIEEMLREVGTNYGEEAPLSMGL 187
Qy 371 -----LSQTSNFWSKRLWYFQHGYYQGGMKLC--WVLOCLAVL-----GLKGT 415
Db 188 SWSPPIEQTS-----ISSGLVIHMGKFRCSMGTVGQELGSLIVOSQCRKRLNVR 237
Qy 416 VKRLANAPTMEEQRLW-----DSNMLIHVV-----KNGPKPLVWLFVKF 455
Db 238 VDAIVNDSSAALLRAYVDPTTRNSLILGTGTNAIHPPVHAIGLGRKRPQGNF--DY 295
Qy 456 VSLVLFNKAVLWFGGVPKGQYALIKADGIPNIYARTMDGVAENSHVRKQNYFYNNCL 515
Db 296 AKHVIINSEMSFGGV-----LPMTRW-----DDILNRTHLRDPYQPLEYMA 338
Qy 516 TGKPLRD-----NCPYLRREAFATLKSQGVVDNLTVSTNFMEE--- 554
Db 339 TGRYLGEIVRLIIVDAVETAQLFGGELPHSMRDA--YSLDTSIVAFIEADTSPFLTASAA 396
Qy 555 --LKARTYTKVILMDHVDLMDPVANELAECLAKQVAPGGIVW-----RSAS 600
Db 397 LQKEHTWSRPPSPEDRULF--LRVCRISKRAAGYLATAHSMCLNREABISOGPPSPS 455
Qy 601 LSPPYABLIQXAGDVRCCRATQGYMDRVNMYSSF 636
Db 456 FKGRDVTVTSGSNSDCLSIACDGSV--INKYPGF 489

RESULT 7
US-11-301-554-1903
; Sequence 1903, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangui, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE, 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03

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; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 2209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-301-554-1903

Query Match 2.8%; Score 97; DB 10; Length 2209;
Best Local Similarity 19.9%; Pred. No. 14;
Matches 110; Conservative 76; Mismatches 226; Indels 140; Gaps 24;

Qy 94 LAKFK--SIYVVDLCHSLCEVAKKAKAGKMNQVVVEADACQAPPEGTATLITFSYSL 151
Db 1626 LMKFSLDTLYVSTAKH---VFEEKLKP---KLLKLTQAKSSTLINKETKITQTIESCL 1678
Qy 152 TMAPPPFNVDQACSYLSQDGLGVADFPYVG--KYDLPRLQMPWRSRFFWRHSIFDIDNID 210
Db 1679 LSIVNPWEVAIAIS--LAQD--IPEGSFKISALFKCLYLAER-----W-----LQNI 1723
Qy 211 IGPERRAYLEQKLERVMEQNTQGSIPYVWMLRDPYVWIGRLPSVGHALHEEVERPMPF 270
Db 1724 SDEKREKAKALLKLIHQYRSSTEAV-----LJAHKLNTTEEYLR-VIG 1767
Qy 271 PPTFLYTSQSWEDPEPDMVMEINPKOTVLTITSGGCNALNLLVQAGOVSVSDCNPAQSA 330
Db 1768 KPAHLIVSLYEHP-----SINQIQNSSGTDYPDIHAAAKE 1803
Qy 331 LLELKKVAIQOLEPEVDYVQLFGE-----GVHPRIEELYE-----KKLAPFLSQT 374
Db 1804 IAE-----VNEINLEKVDMLLEKWLCPSTKPGKEP--SELFQEDREALRRVQVLLLSR 1856
Qy 375 SHNFWSKRLWYFQHGYYQGGMKLCW-----VLQCLAVVLGLGKTVKRLANAPTEBQR 429
Db 1857 PIDYSSRMLFVFATSTTTTLGMHQLTFAHRTALQCL--FYLADKETIESLPKKPIEEVKS 1915
Qy 430 RLMDSNMLIHF-----VKNQPKPLVW-----LFVKPVSULVFNKAV-- 465
Db 1916 YLRCTITFLASFETLNIPIITVELFCSPKEGMKGLKWNHSHESMAVRLVTELCLKEYKIYD 1975
Qy 466 --LWFGGGVPGKQYALIKADGIPNIYARTMDGVAENSHVRKQNYF---YNYCLTGKFL 520
Db 1976 LQLMNG-----LLOKLGLGNMIPYLRKVLKAISSIHSLWQYVPYFSKAWQVRIQPL 2027
Qy 521 RDNCP-----TYLREAAAFATK---SGVDNLTVSTNFFMEELKARTYTKVILMDHVDW 571
Db 2028 SASCPFLSPDQLSDCSSESLIAVLECPVSGDLDLIGVARQYIOLELPAPALACMLMPHSEK 2087
Qy 572 LDMPVANELAEC 583
Db 2088 RHQIQKNFLGSC 2099

RESULT 8
US-10-467-657-7224
; Sequence 7224, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

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; APPLICANT: MONACI Elisabetta
; FILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqmin99, version 1.04
; SEQ ID NO 7224
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7224

Query Match          2.8%; Score 96; DB 9; Length 326;
Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 30; Conservative 21; Mismatches 39; Indels 26; Gaps 6;

QY 120 KGKNVQVVEADACQFAPP---EGTATLITFSYSLTMIPPF-----HNV-IDQACS--- 166
DB 214 EGWLEHEVTRLTVCYKPLADGIDTLVLGCTHFPFLKPLIGRAHNVALVDSAITTAE 273

QY 167 ----YLSQDLGVAD-----FYSGKYDLPLOMPHRSRRFFWRSIFDIDNIDIG 212
DB 274 ETARVLAQEGLLDTCNNPNDRFYVS---DIPLKFTTIGERPLGRTMQIEWVSIG 326

RESULT 9
US-11-115-639-31
; Sequence 31, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-31

Query Match          2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;

QY 214 ERRAY-----LEQKLERVWE---QNTQGSIPYVPLRAPYVYVWIGRLPSVGHALH 260
DB 1775 EERGAYTTLKQAKRMIEQKSNEVWECLQEITEG-----YPLVLLNRAPT---LH 1819
QY 261 EERVERPMPPTFLYTQSWEDPEPDMVEINP----- 294
DB 1820 KQSIQ---AFHPKLI-----DGKAIQLHLVCSAFNADFQDQMAVHVPVLSQBAI 1866
QY 295 -KDTVLTITSGGCNALNLLVQAGOVSDCNPAQSALLELKVAIQOLEFEDVWOLFGE 353
DB 1867 AECKVLMSS-----MNILLPASGRAVAI---PSQDMVLGYLISLEKSGVKGHEKLFSS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSQTSHNFWSKRLWFYQ 387
DB 1919 VNEIITAITDKELDIHAKIRVLDOGNIATTSAGRMIKSIILPDFIPT--DLWNRPMKKD 1976
QY 388 HG-----LYOQGMKGLCWVLOCL-----AVVLGLG-----KTVKRLANAPTWE 426
DB 1977 IGVLVDYVHKVGGIGITATFLDNLKTLGFRYATKAGISISMEDIITTPDKQKQMVKEAKVE 2036
QY 427 EQR--RLWDSNMLHFFKNGPKPLVWLFV-----KFVSLVL-----FNKAVLWFGGVP 473
DB 2037 VKKIQQQYDQGLLTQBERYNKIIDTWTEVNDKMSKEMMTAQAQKEGNSIYMMADSGAR 2096

; APPLICANT: MONACI Elisabetta
; FILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqmin99, version 1.04
; SEQ ID NO 7224
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7224

Query Match          2.8%; Score 96; DB 9; Length 326;
Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 30; Conservative 21; Mismatches 39; Indels 26; Gaps 6;

QY 120 KGKNVQVVEADACQFAPP---EGTATLITFSYSLTMIPPF-----HNV-IDQACS--- 166
DB 214 EGWLEHEVTRLTVCYKPLADGIDTLVLGCTHFPFLKPLIGRAHNVALVDSAITTAE 273

QY 167 ----YLSQDLGVAD-----FYSGKYDLPLOMPHRSRRFFWRSIFDIDNIDIG 212
DB 274 ETARVLAQEGLLDTCNNPNDRFYVS---DIPLKFTTIGERPLGRTMQIEWVSIG 326

RESULT 10
US-11-115-639-32
; Sequence 32, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-32

Query Match          2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;

QY 214 ERRAY-----LEQKLERVWE---QNTQGSIPYVPLRAPYVYVWIGRLPSVGHALH 260
DB 1775 EERGAYTTLKQAKRMIEQKSNEVWECLQEITEG-----YPLVLLNRAPT---LH 1819
QY 261 EERVERPMPPTFLYTQSWEDPEPDMVEINP----- 294
DB 1820 KQSIQ---AFHPKLI-----DGKAIQLHLVCSAFNADFQDQMAVHVPVLSQBAI 1866
QY 295 -KDTVLTITSGGCNALNLLVQAGOVSDCNPAQSALLELKVAIQOLEFEDVWOLFGE 353
DB 1867 AECKVLMSS-----MNILLPASGRAVAI---PSQDMVLGYLISLEKSGVKGHEKLFSS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSQTSHNFWSKRLWFYQ 387
DB 1919 VNEIITAITDKELDIHAKIRVLDOGNIATTSAGRMIKSIILPDFIPT--DLWNRPMKKD 1976
QY 388 HG-----LYOQGMKGLCWVLOCL-----AVVLGLG-----KTVKRLANAPTWE 426
DB 1977 IGVLVDYVHKVGGIGITATFLDNLKTLGFRYATKAGISISMEDIITTPDKQKQMVKEAKVE 2036
QY 427 EQR--RLWDSNMLHFFKNGPKPLVWLFV-----KFVSLVL-----FNKAVLWFGGVP 473
DB 2037 VKKIQQQYDQGLLTQBERYNKIIDTWTEVNDKMSKEMMTAQAQKEGNSIYMMADSGAR 2096
```

QY 474 GK-----QYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNNCLTG--KELR 521
Db 2097 GSAQIROLSAMRGLMTKPDGSIITPTI---ISNFKEGNLVLE-----YFNSTHGARKGLA 2149
QY 522 DNCPTYLREAAAFATLKSGVWNLTVSTNF-----FWEELKAR 558
Db 2150 D---TALKTANAGYLTRKLIID---VSNQVKVSDDCGTHGIEITDIAVGSSELIEPLEER 2203
QY 559 TYTKVILMDHVDLWDMPVANEL---AECL-----AKQVAPGGIVWRSASLSPP 604
Db 2204 IFGRVLLEDDVID---PITNEILLYADTLIDEGAKKVVVEAGI---KSITIRT 2250

RESULT 11
US-11-115-639-33
; Sequence 33, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-33

Query Match 2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;

QY 214 ERRAY-----LEOKLERVWE--ONTQGSIPYVPLRAPYVYVWIGRLPSVGHALH 260
Db 1775 EERGATTLKQAKRMIEQKSNEVWECLOETEG-----YPVILNRAPT-----LH 1819
QY 261 BERVPRPMPFPPTFLYTQSWEDPEPDMVEINP-----DKRAIQHLPLVCSAFNADFDGDMVHVPLSQEAI 1866
Db 1820 KQSIQ---AFHPKLI-----DGRKAIQLHPLVCSAFNADFDGDMVHVPLSQEAI 1866
QY 295 -KDTVLITSGGCNALNLVQAGVSVDCNPAQSALLELKVAIQOLEFEDVWQLPGE 353
Db 1867 AECKVLMLS-----MNLITPASGRAVAI---PSQDMVLGLYLSLEKSGVKGEHKLFS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSQTSHNFWSKELWYFQ 387
Db 1919 VNEIITAIDTKELDIHAKIRVLVDQGNIIATAGRMIIKSIILPDFIPT--DLWNRPMKKD 1976
QY 388 HG-----LYYQGMGKLCWVLQCL-----AVVLGLG-----KTVKRLNAPATME 426
Db 1977 IGVLDVYVHKVGIGITATFDLNLKTLGFRVATKAGISMEDIIITPKDKQKWEKARVE 2036
QY 427 EQR--RLNDSNMLIHVKNQPKPLVWLFV-----KFSVLV-----FNKAVLWFGGVP 473
Db 2037 VKKIQOQYDQGLITDQERYNKIIDTWTVEVNDKMSKEMMTAQAQKEGFSIYMMADSGAR 2096
QY 474 GK-----QYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNNCLTG--KELR 521
Db 2097 GSAQIROLSAMRGLMTKPDGSIITPTI---ISNFKEGNLVLE-----YFNSTHGARKGLA 2149
QY 522 DNCPTYLREAAAFATLKSGVWNLTVSTNF-----FWEELKAR 558

Db 2150 D---TALKTANAGYLTRKLIID---VSNQVKVSDDCGTHGIEITDIAVGSSELIEPLEER 2203
QY 559 TYTKVILMDHVDLWDMPVANEL---AECL-----AKQVAPGGIVWRSASLSPP 604
Db 2204 IFGRVLLEDDVID---PITNEILLYADTLIDEGAKKVVVEAGI---KSITIRT 2250

RESULT 12
US-11-096-568A-2582
; Sequence 2582, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2582
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(658)
; OTHER INFORMATION: Ceres Seq. ID no. 15176030
US-11-096-568A-2582

Query Match 2.7%; Score 94; DB 11; Length 658;
Best Local Similarity 19.6%; Pred. No. 4.5;
Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;

QY 20 EKLKLSMKDDLTVIRHWNFGSKGD-----DHAARLESFYGPAAAFARLAER 69
Db 56 EKLQLAGVSQRCVVL-----GSSKAEDKHLQLVHTKOHVNLVKSISTKQKDYRRNRIASQ 110
QY 70 SNLIWVDLGGGTGENVDMMADYIDLAKFKSIYVVDLCHSLCEVAKKAKAKGWNQVVE 129
Db 111 LNSIY--LNGSSSEAAYLAAG-----SVVKLAEKVAEG-----E 142
QY 130 ADACQFAPPEGTATLITFSYSLTMIPFPHNVIDQACSYLSQDGLGVADVVSQKYDLP 189
Db 143 LD-CGFA-----IVRPPGHAEADAMGFCLFNNVAVAAASFLNERNPDLGV 187
QY 190 RQ---MPW-----SRPFWRSS---IFDIDNIDIGERRAYLEOKLERVWEQNTQCSI 235
Db 188 KKILIVDMDVHHNGTQKMFMKDPRVLFFSVHRHEYGGFYAGDDGYNMVGEGPGEFN 247
QY 236 PYVPWLRAPYVYVWIGRLPSVGHALHEERVERPPW--PPPTFLYTQSWEDPEPD----- 286
Db 248 INVWDQ-----GRGDADYLAANDHILIPVAREFNPVIFLSAGFDAINDPLGGCC 300
QY 287 -----MEVMEINPKDTVLITSGGCNALNLVQAGVSVDCNPAQSALLELK 336
Db 301 VTPYGSVMLKKLMEFAQKIVLAL-EGYN-LDSIAKSSLACVQV-----LLEDKQ 350
QY 337 V--AIQOLEFEDVWQLFEGVHPRI-----BEL-----YEKKLAPFL-----SOTS 375
Db 351 IQGPPEAYPFESTWRVI-QAVRKELCTYWPSLADELSWKLINQKTPTPTIILISSDSETE 409
QY 376 HN-----FWSKRL-----WYFOHG-----L 390
Db 410 DNAOGLLDQMSKLSIENPOGTILLENHQVEPASTSWRADLAKVDVWYASFGSNMMPKPRFLC 469
QY 391 YYQGMGKLCWVLOCLAVVLGLGKTVKRLANAPTMEQRRLWDSNMLIHVKNQPKPLVW 450
Db 470 YIQGGQ-----VDGLKKVC-----VGSMD-----KSPPKETVW 497
QY 451 LFVVFVSLVLEFNK--AVLWFGGYPGKOYALIKADGPIENYIART 494
Db 498 --ETFPHRLFFRGRESSVGMVGGV-----AFTNPLANLIDOT 532

RESULT 13

US-11-096-568A-2581
; Sequence 2581, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thebyd
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2581
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 15176029
; US-11-096-568A-2581

Query Match 2.7%; Score 94; DB 11; Length 660;
Best Local Similarity 19.6%; Pred. No. 4.5;
Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;

Qy 20 EKLKSSMKDDLTVLRLHWMFGSKGD-----DHAARLESFYGPAQAFAARLAER 69
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 58 EKLQAGVSQRVVU-----GSSKAEDKHLQLVHTKDHNVLVKISTKTQKYRNRITASQ 112
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 70 SNLIWDLGGGTGVNDMMADYIDLAKFSIYVDLCHSLCEVAKKKAKGKNVQVE 129
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 113 LNSIY--LNGSSSAAYLAAG-----SVVKLAEKVAEG-----E 144
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 130 ADACQFAPPEGTATLITFSYSLTIPIPPHNVIDOACS YLSQDGLGVADFYVSGKYDIPL 189
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 145 LD-CGFA-----IVRP PGHAADEANMGFCLENNVAVASFLINERPD LGV 189
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 190 RQ---MPW-----SRFFWR-----IFDINDIDIGERRAYLEQKLERVWEONTGSI 235
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 190 KXILIVDWVHHGNGTQMFKWDPRVLFFSVHRHEYGFYPAGDDGYNMVGEGPGEGFN 249
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 236 PYVPWLRAYYVWIGRLPSVCHALHEERVERPPM--FPPTELYTQS WEDPEPD----- 286
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 250 INVWDQ-----GRCGDADYLAAWHILIPVAREPNDFVLSAGFDAINDPLGSCC 302
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 287 -----MEVMENPKDTVTLTSGCNALNLLVQAGOVVSDCNPAQSAALLELK 336
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 303 VTPYGYSVMLKKLMFEAQGIKVLAL-EGGYN-LDSIAKSSLACVQV-----LLEDKQ 352
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 337 V-AIQOLEFDVWQLFGEGVHPRI-----BEL-----YEKKLAPFL-----SQTS 375
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 353 IQGPPEAYPFESTWRVI-QAVRKELCTYWPSLADEL SKWINOKTPTPIILISSDSETE 411
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 376 HN-----FWSKEL-----WYFQHG-----L 390
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 412 DNAQGLLDQMSKLSIENPQGTLLENHQVEPASTSWRADLAKVDVWYASFSGSNMWKPFLC 471
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 391 YYQGMGKCLWLOCLA AVLGLGKT VKRLANAPTWEQRRLWDSNMLITHFVKNGPKPLVW 450
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 472 YIQGGQ-----VDGLKKVC-----VGSMD-----KSPPKVTWV 499
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 451 LFVKVSLVLPFNK--AVLWFQGGVPGQGYALIKADGPIENVIART 494
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 500 --BTFFPHRLFQGRESSGWGVG-----AFTNPPLANLIDQT 534
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :

; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; TITLE OF INVENTION: Therby
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 2580
 ; LENGTH: 680
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(680)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15176028
 US-11-096-568A-2580

Query Match 2.7%; Score 94; DB 11; Length 680;
 Best Local Similarity 19.6%; Pred.No.4.7;
 Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;

Qy	20	EKLSSMKDILTIRHWMFGSKGD-----DHAARLESFYGPQAAFAAALAE	69
Db	78	EKLQAGVQRVVL-----GSSKAEDHQLVHTKDHVNLVKSISTKQDYRNRIASQ	132
Qy	70	SNLIWDLGGGTGVNDMMADYIDIAKFSIYVVDLCHSLCEVAKKAKAKGKKNVQVVE	129
Db	133	LNSIV--LNGSSSEAAVLAAG-----SVVKLAEKVASEG-----E	164
Qy	130	ADACQFAPPEGTATLITFSYSLTWIPPHNVIDQACSVLSQDGLVGVAIFYSGKYDLPL	189
Db	165	LD--CGFA-----IVRPPGHAEADEAMGFLFNNAVVAASFLINERPD LGV	209
Qy	190	RQ---MPW-----SRRFWR-----IFDIDNIDIGPERRAYLEQKLRVWEQNTQGS	235
Db	210	KKILIVDWDVHNGTQXMFWDPRVLF9VHRHEYGGFYAGDDGDYNNVGECPGEGFN	269
Qy	236	PYPWLRAPYYVWITGRLPVSGHALHEERVRPPM--FPPTFLYTQSWEDPEPD-----	286
Db	270	INVPDQ-----GRCGDADYLAADWHILIPVAREFNPDI FLSAGFDAINDPLGGCC	322
Qy	287	-----MEVMEINPKDTVLTITSGGCHALNLLVQAGQVVSVDGNPAQSALLEKK	336
Db	323	VTPYGYVMKLKMEFAQKGTVLAL--EGYN--LDSIAKSSACVQV-----LLEDKQ	372
Qy	337	V--AIQLEPEDVMOLFGEVHPRI-----BEL-----YEKKLAPFL-----SOTS	375
Db	373	IQGPPEAYPESTWRVI--QAVRKRLCTVWPSLADELSWKLINQKTPPTPIILISSDSETE	431
Qy	376	HN-----FWSKRL-----WYFHQG-----L	390
Db	432	DNAQGLLDQMSKLSIENPQGTLLNHHQVEPASTSWRADLKVDMVYASFGSNWKPFLC	491
Qy	391	YYQGGMKLWCVLQCLAVVLGLGKTVKRLANAPTWBEQRRLWDSNMLIHVKNQPKPLVW	450
Db	492	YIQGGQ-----VDGLKKVC-----VGSMD-----KSPPKETVW	519
Qy	451	LFVKFVSLVLENK--AVLWFCGGYPGKQYALIKADGIPENVIART	494
Db	520	--ETFPHRLPFGRESSVGWGVGV-----AFTNPLANLIDQT	554

RESULT 15
 US-11-153-185-7
 ; Sequence 7, Application US/11153185
 ; Publication No. US20060084796A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Feldmann, Kenneth
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA ENCODING
 ; TITLE OF INVENTION: METHYLTRANSFERASES
 ; FILE REFERENCE: 11696/175X01

RESULT 14
US-11-096-568A-2580
; Sequence 2580, Application US11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

GenCore version 5.1.7

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OM protein - nucleic search, using frame, using p2n model

Run on: May 4, 2006, 17:20:40 ; Search time 316 Seconds
(without alignments)
3645.126 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSGRDRPASYYTKNFSLE.....RVNMYSSPYMARRKAKKDN 648

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGHT=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	352	10.2	933	3	US-09-248-796A-7130
2	158	4.6	666	3	US-09-248-796A-12232
3	138.5	4.0	8832	3	US-09-902-540-984
4	126.5	3.7	990	3	US-09-902-540-9203
5	121	3.5	639	3	US-09-107-532A-3600
6	118.5	3.4	1155	3	US-09-439-313-373
7	118.5	3.4	1155	3	US-09-352-616A-373
8	118.5	3.4	1155	3	US-09-289-198-301
9	118.5	3.4	1155	3	US-09-636-215-373

10	118.5	3.4	1155	3	US-09-685-166A-373	Sequence 373, App
11	118.5	3.4	1155	3	US-09-429-755-301	Sequence 301, App
12	118.5	3.4	1155	3	US-09-679-426-373	Sequence 373, App
13	118.5	3.4	1155	3	US-09-759-143-373	Sequence 373, App
14	118.5	3.4	1155	3	US-09-651-236-373	Sequence 373, App
15	118.5	3.4	1155	3	US-09-699-295-301	Sequence 301, App
16	118.5	3.4	1155	3	US-09-534-825A-301	Sequence 301, App
17	118.5	3.4	1155	3	US-09-657-279-373	Sequence 373, App
18	118.5	3.4	1155	3	US-10-012-896-373	Sequence 373, App
19	118.5	3.4	1590	3	US-09-699-295-323	Sequence 323, App
20	118.5	3.4	2000	3	US-09-439-313-374	Sequence 374, App
21	118.5	3.4	2000	3	US-09-352-616A-374	Sequence 374, App
22	118.5	3.4	2000	3	US-09-289-198-302	Sequence 302, App
23	118.5	3.4	2000	3	US-09-636-215-374	Sequence 374, App
24	118.5	3.4	2000	3	US-09-685-166A-374	Sequence 374, App
25	118.5	3.4	2000	3	US-09-429-755-302	Sequence 302, App
26	118.5	3.4	2000	3	US-09-679-426-374	Sequence 374, App
27	118.5	3.4	2000	3	US-09-759-143-374	Sequence 374, App
28	118.5	3.4	2000	3	US-09-651-236-374	Sequence 374, App
29	118.5	3.4	2000	3	US-09-699-295-302	Sequence 302, App
30	118.5	3.4	2000	3	US-09-534-825A-302	Sequence 302, App
31	118.5	3.4	2000	3	US-09-657-279-374	Sequence 374, App
32	118.5	3.4	2000	3	US-10-012-896-374	Sequence 374, App
33	118.5	3.4	2040	3	US-09-439-313-375	Sequence 375, App
34	118.5	3.4	2040	3	US-09-352-616A-375	Sequence 375, App
35	118.5	3.4	2040	3	US-09-289-198-303	Sequence 303, App
36	118.5	3.4	2040	3	US-09-636-215-375	Sequence 375, App
37	118.5	3.4	2040	3	US-09-685-166A-375	Sequence 375, App
38	118.5	3.4	2040	3	US-09-429-755-303	Sequence 303, App
39	118.5	3.4	2040	3	US-09-679-426-375	Sequence 375, App
40	118.5	3.4	2040	3	US-09-759-143-375	Sequence 375, App
41	118.5	3.4	2040	3	US-09-651-236-375	Sequence 375, App
42	118.5	3.4	2040	3	US-09-699-295-303	Sequence 303, App
43	118.5	3.4	2040	3	US-09-534-825A-303	Sequence 303, App
44	118.5	3.4	2040	3	US-09-657-279-375	Sequence 375, App
45	118.5	3.4	2040	3	US-10-012-896-375	Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-248-796A-7130
; Sequence 7130, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7130
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7130

Alignment Scores:
Pred. No.: 6.02e-33 Length: 933
Score: 352.00 Matches: 95
Percent Similarity: 40.5% Conservative: 35
Best Local Similarity: 29.8% Mismatches: 97
Query Match: 10.2% Indels: 94
DB: 3 Gaps: 8

US-10-620-914-45 (1-648) x US-09-248-796A-7130 (1-933)

Qy 144 LeuIleThrPheSerTyrSerLeuThrWetIleProPheHisAsnValIleAspGln 163

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Db 7 TTGATTACTTTTCGTATTCATGTCGATGATCCCACTTTCATGCTGCTATCGATAT 66
Qy 164 AlaCysSerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyrValSer--- 182
Db 67 GCTGTTTCTAAATTAGATATGAAGGTATTATTGCCACTGTAGATTTTGGTATTCAAAGC 126
Qy 183 -----GlyLysTyrAsp-----LeuProLeuArgGlnMetPro 193
Db 127 AGTGACACCTCAATGGGTGCTATTAAATACTGTTGGTGGTTGGTTAAACAGGACATTCCT 186
Qy 194 TrpSerArgAlaGlnPhePheTyrArgSerIlePheAspIleAspAsnIleAspIleGlyPro 213
Db 187 TGGATATTACGTAATTTTGGAGATTTGGTTGAGCTGATAAAGTGTTTTGGATCT 246
Qy 214 GluArgAlaTyrLeuGluGlnLysLeuGluArgValTrpGluGlnAsnThrGln--- 232
Db 247 TCAAGAAGAACTATTTCGAATATAAATTGCTACCGTCAAACTCTTGAATTCATACAAC 306
Qy 233 -----GlySerIleProTyrValProTrpLeuArgAlaProTyrTyrValTrpIle 249
Db 307 AAGGCTTTGGGTAAATC-----CCCTATTATTATTTGGATT 342
Qy 250 GlyArgLeuProSerValGlyHisAlaLeuHisGluGlu-----ArgValGlu 265
Db 343 GGTGTGTGATAATCAAAATCACACACCATTTTAGAAGATTGAATTTGTAGCCACTGAA 402
Qy 266 ArgProProMetPheProThr----- 273
Db 403 TCCGCTTACCTTGCTCCAACTACAACCTCAACTCGCTAATCAACTTGAAGATATTCCAATT 462
Qy 273 ----- 273
Db 463 TCTAAGTGTATGAAGCTGCTTTAATCAACTTGCAAAAAAATTTACCTTACCCATCAATG 522
Qy 273 ----- 273
Db 523 TACTATCAAAAAGGAATATTGGAGAGTCTACTATGATGAATGAATCCATTGTATGAACAA 582
Qy 274 -----PheLeuTyrThrGlnSerTrpGluAspProGluProAspMetGluVal 289
Db 583 TTTAAAAACCAATACATATTATGCTTTTCACTTTGGGAAGATCCTCGTGAAGATCATAAACTT 642
Qy 290 MetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLeu 309
Db 643 TTGAATTTTACCAGTGATGACTGTTTGGCTATTACTTCAGCTGGTGTGAATAATTTTG 702
Qy 310 AsnLeu-----LeuValGlnGlyAlaGlyGlnValValSerValAspCysAsnProAla 327
Db 703 AGTTATGCTAGTTTACCACCAACCACCAAGATTCATGCTGTGTGATCTTAATCCATGT 762
Qy 328 GlnSerAlaLeuLeuGluLeuLysLysValAlaIleGlnGlnLeuGluPheGluAspVal 347
Db 763 CAAACCACTTTATTAGAATTTGAAATTTGGCTAGTTAGATGCTTTCTCTCAAGAACAAT 822
Qy 348 TrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrGluLysLysLeu 367
Db 823 TGGTCAATGTTTGGTGAAGGTAAATTCGAAATTTCAATGATCTTTTGATGATCACTTTG 882
Qy 368 AlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTrpTyrPheGln 387
Db 883 GCGCGGCACATGCTCTTCTAATGCC-----TTCCAA 912
Qy 388 His 388
Db 913 CAC 915
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RESULT 2

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US-09-248-796A-12232
; Sequence 12232, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12232
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-12232

Alignment Scores:
Pred. No.: 2,74e-09 Length: 666
Score: 158.00 Matches: 34
Percent Similarity: 55.7% Conservative: 20
Best Local Similarity: 35.1% Mismatches: 19
Query Match: 4.6% Indels: 24
DB: 3 Gaps: 3

US-10-620-914-45 (1-648) x US-09-248-796A-12232 (1-666)

Qy 51 LeuGluSerPheTyrGlyProGlnAlaAlaAlaPhe----- 62
Db 367 TTAGATGATTCATAAGATCAAGCTCATATTTATGATAACACTAGAGAATTTTGTG 426
Qy 63 -----AlaAlaArgLeuAlaGluArgSerAsnLeu 72
Db 427 AAAGTAGACAAGATGCTTTAGATTAGCTATTTCCCATTTTACCCAAAAGAAATCTT 486
Qy 73 IleTrpValAspLeuGlyGlyThrGlyGluAsnValAspMetMetAlaAspTyrIle 92
Db 487 ATTTGGATAGATATTGGTGGTGGAACTGGTTCCAATATTGAATTCATGATGAAATTAGT 546
Qy 93 AspleuAlaLys---PheLysSerIleTyrValValAspLeuCysHisSerLeuCysGlu 111
Db 547 AAAATATCTGAAAACCTTTTAAAGCTGTTTATTGGTTGATCTTCCCATCTTTTGTGAA 606
Qy 112 ValAlaLysLysLysAlaLysAla-----LysGlyTyrLys 123
Db 607 GTTGCTAAGGCAAGATTTGAATCCCATGATTGACACCCGGGACTGGAAA 657

RESULT 3
US-09-902-540-984/c
; Sequence 984, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 984
; LENGTH: 8832
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-984

Alignment Scores:
Pred. No.: 6,27e-05 Length: 8832
Score: 138.50 Matches: 97
Percent Similarity: 37.7% Conservative: 50
Best Local Similarity: 24.9% Mismatches: 138
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Query Match: 4.0% Indels: 107
DB: 3 Gaps: 17
US-10-620-914-45 (1-648) x US-09-902-540-984 (1-8832)

QY 252 LeuProSerValGlyHisAlaLeuHisGluGluArgValGluArgProProMetPhePro 271
DB 2341 GTTCGAGGTAGAACATGCCAAGAACTGGCCCTGGTTTCAGCCGCCGCCCTT----- 2288
QY 272 ProThrPheLeuTyrThrGlnSerTrpGluAspProGluProAspMetGluValMetGlu 291
DB 2287 ---CGCTTGAAGTTCCCGCTGTCGGGAGGATCGCGCTGGAGTTGGCGCTCGTCGAG 2231
QY 292 IleAsnProLysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLeuAsnLeu 311
DB 2230 CGCAGCGCGCGCGCGCTGCTCAGCTGGCTCGCGCTGGAGTTGCACACTCCTCACCTCG 2171
QY 312 LeuValGln---GlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAla 330
DB 2170 GCGCGCGCCATCCAGCGCTCAGCTGGTGGCTTCGATTTCACCCGCTCAGCTCGCG 2111
QY 331 LeuLeuGluLeuLysValAlaIleGlnGlnLeu-----Glu 343
DB 2110 CATGTCGCGAGAGCGGAGGGCTCGGTCCCTTCGCTGGCGCTACAGCGTGAT 2051
QY 344 PheGluAspValTrpGlnLeu-----PheGlyGluGlyValHisProArg 358
DB 2050 GCGGAGGAGCGCGCGCTGAATCAGCGCGCGAAATTC---GAGGGGCTCTTCGCGCAG 1994
QY 359 IleGluGluLeuTyrGluLysLysLeuAlaProPheLeuSerGlnThrSerHis-AsnPh 378
DB 1993 CTCGCGCGCTCATCGAGGAGTCTCGCGCC-----GCGCATGAAC-- 1951
QY 378 eTrpSerLysArg-LeuTrpTyrPheGlnHisGlyLeuTyrTyrGlnGlyMetGlyL 398
DB 1950 ---TCGCGCGGTCTTCGCGCGCCACCGCTCACAACCGCGGAGGC----- 1902
QY 398 ysLeuCyTrpValLeuGlnCysLeuAlaValLeuGlyLeuGlyLysThrValLysA 418
DB 1901 -CTGTGC----- 1896
QY 418 rgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLeuTrpAspSerAsnMetLeu 438
DB 1895 -----CGCTGG 1889
QY 438 leHisPheValLysAsnGlyProLysProLeuValTrpLeuPheValLysPheValSerL 458
DB 1888 TTCGCTTCGCCCT-ACTGGCGGTGGCTTCGAGCTGGCCCTGGCGGCGCG-CTGCTGA 1831
QY 458 euValLeuPheAsnLysAlaValLeuTrpPheGly-----GlyGlyValProGlyLysG 476
DB 1830 ACACCATGTTGGTCCCGCGGACCCAGCATGCGGCGCGGCTCGGTATCTGCTGCTATT 1771
QY 476 lnTyrAlaLeuIleLysAlaAspGlyIleProIleGluAsnTyrIleAlaargThrMeta 496
DB 1770 TCCAGCGGTCTTCGACGC---GGGCTCCAGCGCGAGGAT----- 1733
QY 496 spGlyValAlaGluAsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeu 516
DB 1732 -----GCGCTCGAATCCCTTCTCCAGCAGCTGCTGC 1699
QY 516 hrGlyLysPheLeuArgAspAsnCysProThrTyrLeuArg---GluAlaIlePheAla- 534
DB 1698 TCGGAGGTACTCGGTGAGGATGCCCCGAGTATCTCCGGCTGAAGCCCGCTGGCGC 1639
QY 535 ---ThrLeuLysSerGlyValValAspAsnLeuThrValSerThrAsnPhePheMetGluG 554
DB 1638 TGACGCTCGTCAGGGCTCGTTGGCGATGTGCGCGCTCGACCGCTTC----- 1589
QY 554 luLeuLysAlaArgThrTyrThrLysValIleLeuMetAspHisVal---AspTrpLeuA 573
DB 1588 -----GACGTATCTGCTCTCCAAACATCTTCGACTGTCGCG 1552
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QY 573 spMetProValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyI 593
DB 1551 AAGACGCGCTGTCGCGAGTGGCGGGGTGCTCGCACGTGAGCGCGCGCGCTTGGC 1492
QY 593 leValIleTrpArg-Ser-----AlaSerLeuSerProPro 604
DB 1491 CGTCCTCATCCGCGAGCTCAACAAACCGCGGACCTTCGCGGCTTCTTCAGCCCGCT 1432
QY 605 TyrAlaGluLeuIleGlnLysAla 612
DB 1431 TCGAGTTTCGATGACGCGCTCGCG 1408

RESULT 4
US-09-902-540-9203
; Sequence 9203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9203
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-9203

Alignment Scores:
Pred. No.: 4,18e-05 Length: 990
Score: 126.50 Matches: 94
Percent Similarity: 37.6% Conservative: 48
Best Local Similarity: 24.9% Mismatches: 131
Query Match: 3.7% Indels: 107
DB: 3 Gaps: 17

US-10-620-914-45 (1-648) x US-09-902-540-9203 (1-990)

QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrpGluAspPro 283
DB 16 GTTTCGACGCGCCCTT-----CGCTTGAAGTTTCGCGCTGTCGCGGAGGATGCC 66
QY 284 GluProAspMetGluValMetGluIleAsnProLysAspThrValLeuThrLeuThrSer 303
DB 67 GCGCTGGAGTTGGCGCTCGTCGAGCGCACGCGGGCGCGGCTGCTCAGCGTGGCCTCG 126
QY 304 GlyGlyCysAsnAlaLeuAsnLeuValGln---GlyAlaGlyGlnValValSerVal 322
DB 127 GGAGTTGCACACTCTCCCTCACCCTGGCGGCGCCATCCAGCTCGAGCTGGTGGGCTTC 186
QY 323 AspCysAsnProAlaGlnSerAlaLeuLeuLeuLysLysValAlaIleGlnGlnLeu 342
DB 187 GATTTCACCCGCTCAGCTCGCGCATGTCGCGGAGAGGCGGAGGCGCTCGGTCGCTT 246
QY 343 -----GluPheGluAspValTrpGlnLeu----- 350
DB 247 CCGCTGGCGCGCTACAGCGTGGATCGGAGACGACGCGCGCCCTGAATCAGCGCGCGAA 306
QY 351 PheGlyGluGlyValHisProArgIleGluGluLeuTyrGluLysLeuAlaProPhe 370
DB 307 TTC---GAGGGGCTCTTCGCGCACGCTCGCGCTTCATCGAGGAGTTCGTGCGGCC--- 360
QY 371 LeuSerGlnThrSerHis-AsnPheTrpSerLysArg-LeuTrpTyrPheGlnHisGlyL 390
DB 361 -----GCGCATGAAC-----TCGCGCGGTCTTCGCGCGCGCCACCGCGCC 402
QY 390 euTyrTyrGlnGlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLeuAlaValVal 410
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Db 645 ATGCAGGAGATGAATGTCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisLenPheTrpS 380
Db 705 AGATGAGTATGGAATACCACTGCTGCATACGCTATCTATAATGAAGATAAATAATTAATGC 764
Qy 380 erLysArgLeuTrpTyr 385
Db 765 CAAGAGCACTGCTCTTAT 781

RESULT 8
US-09-289-198-301
; Sequence 301, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; EARLIER FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-289-198-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-289-198-301 (1-1155)
Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgGlyPhePheTrpArgSerIlePhe 204
Db 204 CTTCCCTCTGTCAGCGGGAGTGGCAAGACAGTGGCGCTCTCGAGA----- 254
Qy 205 AspIleAspAsnIleAspIleGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCAGCAGCACTCTGCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGATGGCGAGTGGTGTGCCACTGCTTCCCTGCTGCAGGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAGAGCAGAGTGGCGCTTGGGGAGACTACGACAGTGCCTTCATGGAGCCACG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGTCGC-----TGGAGAGATCT 419
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Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCGTCT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGGACACATGACGTGACACAGAGGACACAAAGAGGAGTGTCTTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGCACACAGACGATGTCACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLeuLysLysValAlaIleGl 340
Db 600 TGTCTCTTGAC---AACAAAAGAGGACAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisLenPheTrpS 380
Db 705 AGATGAGTATGGAATACCACTGCTGCATACGCTATCTATAATGAAGATAAATAATTAATGC 764
Qy 380 erLysArgLeuTrpTyr 385
Db 765 CAAGAGCACTGCTCTTAT 781

RESULT 9
US-09-636-215-373
; Sequence 373, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TREATMENT OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-636-215-373 (1-1155)
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; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John W.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-429-755-301 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGACAGCAAGCGCTTCTGGAGA-----254
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGCAAGTGGTGTGCTGCACACTGCTCCCTCTCAGCGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGAGCAAGTGGCGCTTGGGAGACATGATGACAGTGCCTTCATGGAGCCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTyr-GluAsp-- 282
Db 396 GTACCACGTCG-----TGGAAGAATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGCAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGGAACAGAGAGCAAGCAAGAGGAGTGTCTCATCTGCG 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCGCCAATGGGAATTCAGAGTAGTAAATCTCTGCTGGACAGACGATGCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysValAlaIleGl 340
Db 600 TGTCTTGTAC---AACAACAAAGAGACAGCTCTGATAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTAAATGTTCCTGGAACATGGCACTGATCCAAATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnHeTrrps 380
Db 705 AGATGAGTATGGAATACCACTCTGCACCTAGCTATCTATATAATGAAGATAAATTAATGGC 764

Qy 380 erLysArgLeuTyrTyr 385
Db 765 CAAAGACTGCTCTTAT 781
RESULT 12
US-09-679-426-373
; Sequence 373 Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-679-426-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGACAGCAAGCGCTTCTGGAGA-----254
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGCAAGTGGTGTGCTGCACACTGCTCCCTCTCAGCGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGAGCAAGTGGCGCTTGGGAGACATGATGACAGTGCCTTCATGGAGCCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTyr-GluAsp-- 282
Db 396 GTACCACGTCG-----TGGAAGAATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGCAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479

Qy	290	t-----GlulleAsnProLysAsp-----	ThrValLeuThrLeu	302
		:::		
Db	480	GCTCAGGGACACTGCTGCGTAAACAAGAGGACAAGCAAAAGAGGACTGCTCTCACTATGCG	539	
Qy	302	rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnVal	320	
		:::		
Db	540	CTCTGCCAATGGGAATTCAGAAGTAGTAAACTCTCTGTGGACAGCAGATGTCAACTTAA	599	
Qy	320	lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleG	340	
		:::		
Db	600	TGTCCTTGAC---AACAAAAAGAGCAGCTCTGATAAAG-----GCCGTACA	644	
Qy	340	nGlnLeuGluPheGluAspValTrrPnLeuPheGlyGluGlyValHisProArgIleG	360	
		:::		
Db	645	ATGCCAGGAAGATGNAATGTCGTTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATCC	704	
Qy	360	uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps	380	
		:::		
Db	705	AGATGAGTATGGAAATACCACTCTGCACCTACGCTATCTATAATGAAGATAAATTAATGCG	764	
Qy	380	erLysArgLeuTrrTyr	385	
Db	765	CAAAAGCACTGCTCTTAT	781	

RESULT 13

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US-09-759-143-373
; Sequence 373, Application US/09759143
; Patent NO. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Steiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-373

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Alignment Scores:	
Pred. No.:	0.000529
Score:	118.50
Percent Similarity:	37.4%
Best Local Similarity:	29.1%
Query Match:	3.4%
DB:	3
Gaps:	11
Indels:	61
Mismatches:	81
Conservative:	19
Matches:	66
Length:	1155

US-10-620-914-45 (1-648) X US-09-759-143-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTipArgSerIlePhe 204
Db 204 CTTCCCTGCTGAGGGGAGTGCAAGAGCAACGTTGGCGCTCTGGAGA-----254

Qy	205	AspIleaspAenIleaspIleGlyProGluArgArgAlaTyLeuGluGlnLysLeuGlu	224
Db	255	-----CCAGCAGCAGCTCTGCTAT-----GAA	275
Qy	225	ArgValTrpGluGlnAenThrGlnGlySerIleProTyValProTrpLeuArgAlaPro	244
Db	276	GACACTCAGGAAACAAGATGGGCAAGTGGTGTGCCACCTGCTTCCCTGTGCAGGGGGAG	335
Qy	245	TyrTyValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg	263
Db	336	CGGCAAGAGCAAGGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCGAG	395
Qy	264	ValGluArgProProMetPheProProThrPheLeuTyThrGlnSerTrp-GluAsp--	282
Db	396	GTACCACGCTCCG-----TGGAAGAGATCT	419
Qy	283	-----ProGluProAspMetGluValMe	290
Db	420	GGACAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAGAAAGATCTCATCGTCAT	479
Qy	290	t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh	302
Db	480	GCTCAGGGACACTGACGTGAAACAAGAGGACGAAGCAAAAGAGGACTGTGCTCTACATCTGGC	539
Qy	302	rSex-----GlyGlyCysAenAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValVa	320
Db	540	CTCTGCCCAATGGGAATTTCAGAAAGTAGTAAAACTCTCTGGACAGACGATGCAACTAA	599
Qy	320	lSerValAspCysAenProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGl	340
Db	600	TGTCCTTGAC---AACAAAAGAGGACAGCTCTGATAAG-----GCCGTACA	644
Qy	340	nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl	360
Db	645	ATGCCAGGAAGATGAATGTGGTAAATGTGTGCGAATGSCACTGTATCCAAATATCC	704
Qy	360	uGluLeuTyTr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAenPheTrpS	380
Db	705	AGATGAGTAGTGAATAATACCACCTCTGCACCTACGCTATCTATAATGAAGATAAATTAATGGC	764
Qy	380	erLysArgLeuTrpTyTr	385
Db	765	CAAAAGCACTGCTCTTAT	781

RESIII.T 14

US-09-651-236-373
 ; Sequence 373, Application US/09651236
 ; Patent No. 6818751
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqui
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.42718C18
 ; CURRENT APPLICATION NUMBER: US/09/651,236
 ; CURRENT FILING DATE: 2000-08-29
 ; NUMBER OF SEQ ID NOS: 865

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-651-236-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGAGCAACGTGGCGCTTCTGGAGA----- 254
Qy 205 AspileAspAenileAspileGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTrrpGluGlnAsnThrGlnGlySerileProTyrValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGAGTGGCAAGTGGTGTGCCTCTCCCTGCTGCAGGGGAG 335
Qy 245 TyrTyrValTrrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGTCGG-----TGGAAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAAGTCCACAGAGTGGCTGGTGGGTAAAGTCCCAGAAAGGATCTCATCGTCAT 479
Qy 290 t-----GluileAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGCTGAACAAGAGCAAGCAAGCAAGAGGAGGACTGCTCTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGCTGGACAGACGATGTCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleGl 340
Db 600 TGTCTTTGAC---AACAAAAGAGGACAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTTAAATGTGTGGAAACATGGCACTGTATCCAAATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAAATACCACCTCTGCACTATCTATATAATGAAGAATAAATTAATGCG 764
Qy 380 erLysArgLeuTrrpTyr 385
Db 765 CAAGCACTGCTCTTAT 781
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RESULT 15

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US-09-699-295-301
; Sequence 301, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
```

```
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; CURRENT FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-699-295-301 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGAGCAACGTGGCGCTTCTGGAGA----- 254
Qy 205 AspileAspAenileAspileGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTrrpGluGlnAsnThrGlnGlySerileProTyrValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGAGTGGCAAGTGGTGTGCCTCTCCCTGCTGCAGGGGAG 335
Qy 245 TyrTyrValTrrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGTCGG-----TGGAAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAAGTCCACAGAGTGGCTGGTGGGTAAAGTCCCAGAAAGGATCTCATCGTCAT 479
Qy 290 t-----GluileAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGCTGAACAAGAGCAAGCAAGCAAGAGGAGGACTGCTCTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGCTGGACAGACGATGTCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleGl 340
Db 600 TGTCTTTGAC---AACAAAAGAGGACAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTTAAATGTGTGGAAACATGGCACTGTATCCAAATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAAATACCACCTCTGCACTATCTATATAATGAAGAATAAATTAATGCG 764
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Qy 380 erLysArgLeuTrpTyr 385
|||
Db 765 CAAGCACTGCTCTTAT 781

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2006, 17:40:29 ; Search time 1360 Seconds
(without alignments)
3940.115 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSRGDRPASVTKNFSL.....RVNMYSSFYMARRGAKKDN 648

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB pool/US10620914/runat 04052006 130316 18884/app_query.fasta_1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blom62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US10620914 @CGN 1 1 1026 @runat 04052006 130316 18884 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=0 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3463	100.0	1947	7	US-10-620-914-44
2	2838	82.0	5242	7	US-10-620-914-43
3	891	25.7	2259	8	US-10-741-849-6021
4	850.5	24.6	2727	7	US-10-620-914-49
5	804	23.2	3427	7	US-10-620-914-48
6	379.5	11.0	1252	5	US-10-118-495-1
7	379.5	11.0	1252	5	US-10-620-914-1

8	329	9.5	1248	5	US-10-118-495-22	Sequence 22, Appl
9	329	9.5	1248	7	US-10-620-914-28	Sequence 22, Appl
10	326.5	9.4	1251	5	US-10-118-495-28	Sequence 28, Appl
11	326.5	9.4	1251	7	US-10-620-914-28	Sequence 28, Appl
12	292.5	8.4	1251	5	US-10-118-495-32	Sequence 32, Appl
13	292.5	8.4	1251	7	US-10-620-914-32	Sequence 32, Appl
14	128	3.7	4246	6	US-10-085-959-12	Sequence 52, Appl
15	123	3.6	7119	8	US-10-684-141-57	Sequence 57, Appl
16	123	3.6	7119	9	US-10-810-486-57	Sequence 34, Appl
17	120	3.5	666	5	US-10-118-495-34	Sequence 34, Appl
18	120	3.5	666	7	US-10-620-914-34	Sequence 34, Appl
19	119	3.4	6912	8	US-10-335-053-309	Sequence 309, Appl
20	119	3.4	6912	8	US-10-684-141-53	Sequence 53, Appl
21	119	3.4	6912	9	US-10-810-486-53	Sequence 53, Appl
22	119	3.4	6912	9	US-10-887-553A-400	Sequence 400, Appl
23	118.5	3.4	1155	3	US-09-825-301-5	Sequence 5, Appl
24	118.5	3.4	1155	3	US-09-759-143-373	Sequence 373, Appl
25	118.5	3.4	1155	3	US-09-780-669-373	Sequence 373, Appl
26	118.5	3.4	1155	3	US-09-810-936-301	Sequence 301, Appl
27	118.5	3.4	1155	3	US-09-822-827-373	Sequence 373, Appl
28	118.5	3.4	1155	3	US-09-429-755-301	Sequence 301, Appl
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30	118.5	3.4	1155	3	US-09-895-793-373	Sequence 373, Appl
31	118.5	3.4	1155	3	US-09-895-814-373	Sequence 373, Appl
32	118.5	3.4	1155	5	US-10-012-896-373	Sequence 373, Appl
33	118.5	3.4	1155	5	US-10-010-940-373	Sequence 373, Appl
34	118.5	3.4	1155	6	US-10-212-679-301	Sequence 301, Appl
35	118.5	3.4	1155	6	US-10-144-678A-373	Sequence 373, Appl
36	118.5	3.4	1155	6	US-10-033-527-5	Sequence 5, Appl
37	118.5	3.4	1155	6	US-10-294-025-373	Sequence 373, Appl
38	118.5	3.4	1155	7	US-10-079-137B-301	Sequence 301, Appl
39	118.5	3.4	1185	3	US-09-924-400-335	Sequence 335, Appl
40	118.5	3.4	1185	6	US-10-212-679-335	Sequence 335, Appl
41	118.5	3.4	1185	7	US-10-079-137B-335	Sequence 335, Appl
42	118.5	3.4	1383	3	US-09-905-673-64	Sequence 64, Appl
43	118.5	3.4	1383	6	US-10-096-319-64	Sequence 64, Appl
44	118.5	3.4	1434	3	US-09-905-673-65	Sequence 65, Appl
45	118.5	3.4	1434	6	US-10-096-319-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-10-620-914-44
; Sequence 44, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-44

Alignment Scores:					
Pred. No.:	0	Length:	1947		
Score:	3463.00	Matches:	648		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	100.0%	Indels:	0		
DB:	7	Gaps:	0		
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Qy 21 LysLeuLysLeuSerSerMetLysAspAspLeuThrValLeuAraGHisMetTyrPheGly 40
Db 61 AAGCTCAAGCTCAGCAGCATGAGAGATGACCTGACCGTTCCTGCCCATATGTGGTTCGGC 120
Qy 41 SerLysLysGlyAspAspHisAlaAalaArgLeuGluSerPheTyrGlyProGlnAlaAla 60
Db 121 AGCAAGAAGGGCGATGATACGCTGCTCGCTGGAGAGCTTCTACGGCGCCCGAGCGCGCT 180
Qy 61 AlaPheAlaAlaAraGLeuAlaGluAraGSerAsnLeuIleTyrValAspLeuGlyGly 80
Db 181 GCCTTTGTGCTGCCCGCTGGCGAGCGCTCGAACCTCATCTGGGTGACCTGGGTGGTGGC 240
Qy 81 ThrGlyGluAsnValAspMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIle 100
Db 241 ACTGGGAGAGATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGTTCAAGTCCATC 300
Qy 101 TyrValValAspLeuLysHisSerLeuCysGluValAlaLysLysLysAlaLysAlaLys 120
Db 301 TACGTGGTGCACCTGTGCCACTGCTGTGGAGGTGGCCAAAGAAAGAGCGCAAG 360
Qy 121 GlyTyrLysAsnValGlnValAlaGluAlaAspAlaCysGlnPheAlaProGluGly 140
Db 361 GGCTGGAGAGATGCTCAGGTGCTGGAGCGCCAGCGCTTGCCAAATTTGGCGCCCTTGAGGGC 420
Qy 141 ThrAlaThrLeuIleThrPheSerTyrSerLeuThrMetIleProProPheHisAsnVal 160
Db 421 ACCGGAGCTCATCACCTTCTCCTACTCGCTCAGATGATCCACCGTTCCACACAGTC 480
Qy 161 IleAspGlnAlaCysSerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyr 180
Db 481 ATCAGACAGGCTGCTCGTCTGTCCAGACGGCTGGTGGGGCTTGTCCGACTTCTAC 540
Qy 181 ValSerGlyLysTyrAspLeuProLeuArgGlnMetProTyrSerArgArgPhePheTyr 200
Db 541 GTGAGCGGCAAGTACGACCTGCCCTCGCGCCAGATGCCCTGGTGGCGCGTTCTTCCTCG 600
Qy 201 ArgSerIlePheAspIleAspAsnIleAspIleGlyProGluAraGArgAlaTyrLeuGlu 220
Db 601 CGATCGATCTTCGACATCGACAACATTCACATCGGCCCGGAGCGCGCTACCTGGAG 660
Qy 221 GlnLysLeuGluAraGValTyrGluGlnAsnThrGlnGlySerIleProTyrValProTyr 240
Db 661 CAGAAGCTGGAGCGCGCTGTGGAGCAGAACACCCAGGGTTGATCCCCCTACGTGCGGTGG 720
Qy 241 LeuArgAlaProTyrTyrValTyrIleGlyArgLeuProSerValGlyHisAlaLeuHis 260
Db 721 CTGGCGCCCGCTACTACGTGTGGATTGGCCCGCTGGCCAGCGTTGGCCAGCGCTGGAC 780
Qy 261 GluGluAraGValGluArgProMetPheProProThrPheLeuTyrThrGlnSerTyr 280
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Qy 281 GluAspProGluProAspMetGluValMetGluIleAsnProLysAspThrValLeuThr 300
Db 841 GAGGACCCCGAGCGCGATATGGAGGTGATGGAGATCAACCCCAAGGACACGCGTGTGAC 900
Qy 301 LeuThrSerGlyGlyCysAsnAlaLeuAsnLeuValGlnGlyValAlaGlyGlnValVal 320
Db 901 CTGACTACGGCGGGCTGCAATGCCCTGAACTGCTGGTGGAGGGGGCGCGAGGTGGT 960
Qy 321 SerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGln 340
Db 961 TCGGTGGACTGCAACCCCGCGAGTCGGCGCTTCTGGAGCTGAGAAGGTGGCCATTCCAG 1020
Qy 341 GlnLeuGluPheGluAspValTyrGlnLeuPheGlyGluGlyValHisProArgIleGlu 360
Db 1021 CAGCTGGAGTTTGGACGCTGTGGAGCTGTTGGCGAGGGCGGTGCACCCGCGATTGAG 1080

Qy 361 GluLeuTyrGluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPhetripSer 380
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Qy 381 LysArgLeuTyrPheGlnHisGlyLeuTyrTyrGlnGlyGlyMetGlyLysLeuCys 400
Db 1141 AAGCGCTCTGGTACTTCCAGCAGCGCTGTACTACAGGGCGCATGGGCAAGCTGTGC 1200
Qy 401 TrpValLeuGlnCysLeuAlaValLeuGlyLeuGlyLysThrValLysArgLeuAla 420
Db 1201 TGGTGTCTGAGTGCCTGGCGCTGTGGATCGGCAAGCGTCAAGCGCTCGCC 1260
Qy 421 AsnAlaProThrMetGluGlnAraGArgLeuTyrAspSerAsnMetLeuIleHisPhe 440
Db 1261 AACCGGCCACANATGGAGGACGCGCTGTGTGGACAGCAATGCTCATCCACTTC 1320
Qy 441 ValLysAsnGlyProLysProLeuValTyrPhePheValLysPheValSerLeuValLeu 460
Db 1321 GTGAAGAACGGGCCCAAGCGCTGTGTGTGTCTGTTCTGTTCAAGTTCTGTGAGCTGTGTCTC 1380
Qy 461 PheAsnLysAlaValLeuTyrPheGlyGlyValProGlyLysGlnTyrAlaLeuIle 480
Db 1381 TTCAACAAAGCGCTGTGTGTTCGGCGCGCGCTGTGGGCAAGAGTAGCGCTGATC 1440
Qy 481 LysAlaAspGlyIleProIleGluAsnTyrIleAlaArgThrMetAspGlyValAlaGlu 500
Db 1441 AAGCGGACGCGATCCCATTTGAGAACTACATCGCGCGCACCATGGACGGCGTGGCGGAG 1500
Qy 501 AsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeu 520
Db 1501 AACTCGCAGCGTGGCAAGCAGAACTACTTCTTACTACAACTGCCTCACCGGCAAGTTCTCTG 1560
Qy 521 ArgAspAsnCysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyVal 540
Db 1561 CGCACAACTGCCCCACCTACCTCGCGAGCGCGCTTCGCCACCTCAAGAGTGGCGTG 1620
Qy 541 ValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLysAlaArgThrTyr 560
Db 1621 GTGGACAACTGACCGTCTCCACCACTTCTTCATGGAGGAGCTCAAAGCGCGCACCTAC 1680
Qy 561 ThrLysValIleLeuMetAspHisValAspTyrPheLeuAspMetProValAlaAsnGluLeu 580
Db 1681 ACCAAGGTGATTCTGATGGACACGCTGGACTGGCTGGATATGCCCGTGGCCCAACGAGCTG 1740
Qy 581 AlaGluCysLeuAlaLysGlnValAlaProGlyLysIleValIleTyrArgSerAlaSer 600
Db 1741 GCCAGTGCCTGGCCAAAGCAGGTTGGCGCGGCGCATCGTCACTGTGGCTTCGCCCTCC 1800
Qy 601 LeuSerProTyrAlaGluLeuIleGlnLysAlaGlyPheAspValArgCysIleArg 620
Db 1801 CTCAGCGCGCTACGCGGAGCTGATCCAGAAGCGGGCTTCGACGTGCGTGCATCCGC 1860
Qy 621 ArgAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSerSerPheTyrMetAlaArg 640
Db 1861 CGCGCCACTCAGGGCTACATGGACCGCTCAACATGTACAGTCTCTTCTATATGATGCCCGC 1920
Qy 641 ArgLysGlyAlaLysLysAspAsn 648
Db 1921 CGGAAGGGCGCCCAAGAGGCAAC 1944

RESULT 2

US-10-620-914-43

; Sequence 43, Application US/10620914

; Publication No. US20040093639A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; FILE REFERENCE: MSU-07769

; CURRENT APPLICATION NUMBER: US/10/620,914

; CURRENT FILING DATE: 2003-07-16

; PRIOR APPLICATION NUMBER: 10/118,495

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; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 5242
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-43

Alignment Scores:
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Score: 2838.00 Matches: 645
Percent Similarity: 45.6% Conservative: 0
Best Local Similarity: 45.6% Mismatches: 3
Query Match: 82.0% Indels: 771
DB: 7 Gaps: 11

US-10-620-914-45 (1-648) x US-10-620-914-43 (1-5242)

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Qy 21 LysLeuLysLeuSerSerMetLysAspAspLeuThrValLeuArgHisMetTrpPheGly 40
Db 561 AAGCTCAAGCTCAGCAGCATGAAGATGACCTGACCGCTTCGCGCCATATGTGTGGC 620

Qy 41 SerLysLysGlyAspAspHisAlaAlaArgLeuGluSerPheTyrGlyProGlnAlaAla 60
Db 621 AGCAAGAAGGGGATGATGATCGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGGCGCT 680

Qy 61 AlaPhe----- 62
Db 681 GCCTG-TAAGTCGGGATTAACTTTATGTCTCATTTAAGTGTTCGAGTTGCTTACGCGCTG 739

Qy 62 ----- 62
Db 740 TCTGCCCCGGCAGATGCTTTTCGGTTCGGTTCCTCTCGGGTCGAGGCCCATGCTC 799

Qy 63 -----AlaAlaArgLeuAlaGluArgSerAsnLeuIleTrpValAspLeuGlyGly 79
Db 800 GCTGCAATGTGTCGCCGCTGCGCGAGCGCTCGAACCTCATCTGGTTGACCTGGGTGT 859

Qy 80 GlyThrGly----- 82
Db 860 GGCACCTGGGTGAGTCGCGGTTGTATCGGGAGGTGCGGATAGCCCTGCGCGTTGGCT 919

Qy 83 -----GluAsnVal 85
Db 920 GCGCTCGCGCCATTATGCTGATCTGCGCTTTGCTTTTGTGCGCGCAGAGAAATGTC 979

Qy 86 AspMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIleTyrValValAspLeu 105
Db 980 GATATGATGGCTGATTATACATCGACTGGCGAAGTTCAAGTCCATCTACGTGTGACCTG 1039

Qy 106 CysHisSerLeuGluValAlaLysLysLysAlaLysAlaLysGlyTrpLysAsnVal 125
Db 1040 TGCCACTCGCTGTCGAGGTGGCACAAGAAGGCGAAGGCAAGGCTGGAAGAAATGTC 1099

Qy 126 GlnValValGluAlaAspAlaCysGlnPheAlaProProGluGlyThrAlaThrLeuIle 145
Db 1100 CAGTCTGTTGAGGCGCGCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCT 1159

Qy 146 ThrPheSerTyrSerLeuThrMet----- 153
Db 1160 ACCTTCTCTACTCGCTCAGCAG-TGAGTTGCAAGCGCGCTGCGACTTGCCATCGGAGGATC 1218

Qy 154 -----IlePro 155
Db 1219 CATCCACCCACAACGTTTCATCCCTCTCACCCCGCGCTTTTGTGTTGTCAGTGATTTCCA 1278

Qy 156 ProPheHisAsnValIleAspGlnAlaCysSerTyrLeuSerGlnAspGlyLeuValGly 175
Db 1561 ATGGGGTCGGGTCGTGACGGCGCGCTCGAGCTACACCAAGAAGAACTTCTCCCTGGAG 560
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Db 1279 CCGTTCACAACGTCATCGACCGCTTGTCTGTAACCTGTCCTCCCAAGACGGCCTGGTGGC 1338
Qy 176 ValAlaAspPheTyrValSerGlyLysTyrAspLeuProLeuArgGlnMetProTrpSer 195
Db 1339 GTTCCGACCTTCTAGCTGAGCGGCAAGTACGACCTGCGCCTGCGCCAGATGCCCTGGTGC 1398
Qy 196 ArgArgPhePheTrp----- 200
Db 1399 CGCGCTTCTTCTGCGGTGAGTTACCAGGCCGCGCTACACATCTCTCAAGCAAGCGTA 1458
Qy 200 ----- 200
Db 1459 GCTGAGCGGGGCACAGAAGCGCTTAGGGCCCGGGTGGCTTCTGGGTAGTGGCAAGA 1518
Qy 200 ----- 200
Db 1519 TATCGCAAGGCCCTTTCAGCTACCCGAGGTACCATGTATGTCCTCGGACGCTCATCAC 1578
Qy 200 ----- 200
Db 1579 GGTGCTGACTGAGGCACGTGCTCGAGTCTGCGGTCTCATAGGGCTTTTCAGCACATACA 1638
Qy 200 ----- 200
Db 1639 GCGCAGTCTCGAATGCGGTGCTGTCAGCGGTGATGTCCTCGGGACAGCACCATGCACCGT 1698
Qy 200 ----- 200
Db 1699 GCGCGCTTCTTGACTTGCATCCGCTGCTCTGCGGCCCTCCCTGGTTCGCTCAGACACGT 1758
Qy 201 -----ArgSerIlePheAspIleAsn 208
Db 1759 CTCGCTGCCCCGTGTGTCTGCTGCTGCTGTCAGATCGATCTTCGACATCGACAAAC 1818
Qy 209 IleAspIleGlyProGluArgAlaTyrLeuGluGlnLysLeuGluValTrpGlu 228
Db 1819 ATTGACATCGCCCCGAGCGCGCTTACTGTGAGCAGAAGCTGGAGCGCGCTGTGGAG 1878
Qy 229 GlnAsnThr----- 231
Db 1879 CAGAACACCCAGGTGTGTGCGCGTGTGACACCTGCGCTGTGCAAGCCCAAGTAAGTTTG 1938
Qy 231 ----- 231
Db 1939 CTCATCAGCCCTGACAGCACCAGCGCGGTGCGGGATATTCATCGGACAGACCGTCCGCA 1998
Qy 232 -----GlnGlySerIlePro 236
Db 1999 CTGTTGTTAATCCACACGCTCCGCTGCTTCTCTGCGTGTTCAGGGTTCGATCCCC 2058
Qy 237 TyrValProTrpLeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerValGly 256
Db 2059 TAGTGCGGTGGCTGCGCGCCCCCTACTAGTGTGGATTGCGCGCTGCGCCAGCGTTGGC 2118
Qy 257 His----- 257
Db 2119 CG-TGAGTTCGCTGCGCGGGACCTCGTCGCAATCAGGACACATGTTTACGGGGCCCTCA 2177
Qy 257 ----- 257
Db 2178 GTGAGCGTATCGTATCGTTGCACTGTCTGCAAGCGGTACCAAGCGCGCTCCCTTG 2237
Qy 257 ----- 257
Db 2238 CGCGTTGAATTTGTTGGCGCAAGCATGACGCGTGGCGCGATGCCCAACTCGCGTTGAC 2297
Qy 258 -----AlaLeuHisGluGluArgValGluArgProProMetPheProProThrPhe 274
Db 2298 CCTGCAGACGCGCTGACGAGGAGCGGTGAGCGCGCGCCCATGTTCCCGCCACCTTC 2357
Qy 275 LeuTyrThrGlnSerTrpGluAspProGluProAspMetGlu----- 288
Db 2358 CTGTACCGCAGTGTGGGAGGAGCCCCCGAGCCGATATGGAGGTGAGCGGCTCAGCCTGA 2417
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Qy	288	-----	288	Qy	439	HisPheVallysAenGlyProLysProLeuValTrpLeuPheValLysPheValSerLeu	458
Db	2418	GGCAGATACGCAGAAAGAAACGCTCGTGTGTACCCCGAGGGCGGGATACGCACGTTGCGG	2477	Db	3498	CACCTTCGTGAGAACGGGCCCAAGCCGCTGGTGTGGCTGTTCTGTCAGTTCGTGAGCCTG	3557
Qy	288	-----	288	Qy	459	ValLeuPheAenLysAlaValLeuTrpPheGlyGlyValProGlyLysGlnTyrAla	478
Db	2478	AAGCATTTGGCAGCGGTACATCGTCGCACCAGCAAGCAAGCACTAAGCACCGCGTT	2537	Db	3558	GTGCTCTTCAACAGGCGGTGCTGTGGTTCGGCGGCGCGTGCCTGGGCAAGCAGTACGCG	3617
Qy	288	-----	288	Qy	479	LeuIleLysAlaAspGlyIleProIleGluAenTyrIleAlaArgThrMetAspGlyVal	498
Db	2538	CTGTGGGCAATGTGCCACCGCAATGCCTGGCGAGTGGCGAGCTTCGCATTAGTGTATGCC	2597	Db	3618	CTGATCAAGCGGACCGCATCCCCATTGAGAACTACATCGCGCCACCATCGAGCGCGTG	3677
Qy	288	-----	288	Qy	499	AlaGluAenSerHisValArgLysGlnAenTyrPheTyrTyrAenCysLeuThrGlyLys	518
Db	2598	AGTATCAGCCCTAGCTCAGCCTGCAAGCTGTCTGTCTGTAGTGTGTGTGTGTGTGTGTGT	2657	Db	3678	GGCGAGAACTCGCAGCTGGCGACGAACTACTTCTTACTACAACTGCCTCACCGGCAAG	3737
Qy	289	-----ValMe	290	Qy	519	PheLeuArgAspAenCysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSer	538
Db	2658	GAGCGCGNACTCCTGCTGAAACTGTGCTGCCATCCTCTCGTGCCTTCCCAGGTGAT	2717	Db	3738	TTCTGCGCGACAACTGCCACCTAGCTGCGCAGGCGGCTTCGCCACCTCAAGAGT	3797
Qy	290	tGluIleAenProLysAspThrValLeuThrLeuThrSerGlyGlyCysAenAlaLeuAs	310	Qy	539	GlyValValAspAenLeuThrValSerThrAenPhePheMetGluGluLeuLysAlaArg	558
Db	2718	GGAGATCAACCCCAAGGACACGGTGTGACCTGACTAGCGCGGCTGCAATGCCCTGAA	2777	Db	3798	GGCGTGTGTGACAACTGACCGTCTCCACCAACTTCTTCATGGAGAGAGCTCAAAGCGCGC	3857
Qy	310	nLeuLeuValGlnGlyAlaGly	317	Qy	559	ThrTyrThrLys	562
Db	2778	CCTGCTGTGAGGGGCGCGCCAGGTGAGATCATAGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2837	Db	3858	ACCTACCAAGGTTGGGACGAGCGGAGAGTGTGAAAGCGGAGATGCGCGCGGTG	3917
Qy	317	-----	317	Qy	562	-----	562
Db	2838	TCCTTACTTATGATGGCCGCTGCACGGAATGTTAGGAGCGGTTGGCATACATGTAGCT	2897	Db	3918	TAGTGATGCGGAACGCTTGTCTGCCAGGTTGAAAGCGAGCGAGCGAGGAAACGGAATT	3977
Qy	318	-----GlnValValSerValAspCysA	325	Qy	562	-----	562
Db	2898	GCAGAAATGCTGACGTCGCTTTCGGGCTGCTGCTGACAGTGTGTGCGTGGACTGCA	2957	Db	3978	TCAGAAATTCGGATGGCTGGGAAGCGGAAACGAAACAGAAACGGAATAGAGGCCGCTGCGC	4037
Qy	325	snProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGlnGlnLeuGluPheG	345	Qy	562	-----	562
Db	2958	ACCCGCGCAGTCGGCGCTTCTGAGCTGAAGAGGTGGCCATTGAGAGCTGGAGTTTG	3017	Db	4038	AGAACTGGTGGTGGGTTTGGCATCCAGTCTGCCAGGCGCCCGCTGCTACCTGCT	4097
Qy	345	luAspValTrp	348	Qy	563	-----Val	563
Db	3018	AGGAGCTGTGCGAGGTAAAGGGCTCCTCATCTGGGCGCTAGGGACTGCACACGCTGTTG	3077	Db	4098	CAGGTCCGCTTAACCGTTTAAACCCCTCCGCTCACCGCCCCCCCCCCCCCAGAGTG	4157
Qy	348	-----	348	Qy	564	IleLeuMetAspHisValAspTrpLeuAspMetProValAlaAenGluLeuAlaGluCys	583
Db	3078	CTACTGTATGAAACATGCGGGACCTGTGTGAGGCTTGGCGCATTCGCACTGCGATGCTG	3137	Db	4158	ATTCGTGATGGACCACTGGACTGGCTGATATGCCCTGGCCAAACGAGCTGGCCGAGTGC	4217
Qy	348	-----	348	Qy	584	LeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAlaSerLeuSerPro	603
Db	3138	TCCCCCGAGGTCAGACATCCTCTCGCCGGGTGCAACGGCACAGCCCTTTTACATCC	3197	Db	4218	CTGGCCAAAGCAGGTTGCCCGGGCGGCATCGTCATCTGGCGCTCCGCTCCCTCAGCCCG	4277
Qy	349	-----GlnLeuPheGlyGluGlyValHisProArg	358	Qy	604	ProTyrAlaGluLeuIleGlnLysAlaGlyPheAspValArgCysIleArgArgAlaThr	623
Db	3198	GCAACCCCTGTCTGGTAAATCCCTTCCACAGCTGTTCCGGGAGGGGTGCACCCGGC	3257	Db	4278	CCCTACGCGAGCTGATCCAGAGCGGGCTTCGACGTGCTGCTGCATCCGCGCGCCACT	4337
Qy	359	IleGluGluLeuTyrGluLysLysLeuAlaProPheLeuSerGlnThrSerHisAenPhe	378	Qy	624	GlnGlyTyrMetAspArgValAenMetTyr	633
Db	3258	ATTGAGGAGCTGTACGAGAAAGCTGGCGCCCTTCTGTCGCAAAACGAGCCACAACTTC	3317	Db	4338	CAGGCTACATGGACCGCGTCAACATGTACAGGTGCGTGTTCCTGCGAGGTGTGAG	4397
Qy	379	TrpSerLysArgLeuTyrTrpPheGlnHisGlyLeuTyrTyrGlnGlyMetGlyLys	398	Qy	633	-----	633
Db	3318	TGGTCCAAAGCCCTCTGTGTACTTCCAGCACCGCTGTACTACAGGGCGGATGGGCAAG	3377	Db	4398	GATGTAGGATGTCAGTGTGGCGGGAGGAGCATCGGGTTCGAATGGGAGGAGGTTCGT	4457
Qy	399	LeuCysTrpValLeuGlnCysLeuAlaValValLeuGlyLeuGlyLysThrValLysArg	418	Qy	633	-----	633
Db	3378	CTGTGCTGGGTGCTGCACTGCTGGCGTGTGTGTGGGACTGGGCAAGACCGTCAAGCGC	3437	Db	4458	TATTGATCCCGATGGACCTGGGTGATGCGGTGACGCGCTACCGTATGTATGTGCCAAGAC	4517
Qy	419	LeuAlaAenAlaProThrMetGluGluGlnArgArgLeuTrpAspSerAenMetLeuIle	438	Qy	633	-----	633
Db	3438	CTCGCAACGGGCCCAATGGAGGAGCAGCGCCGCTGTGTGGGACAGCAACATGCTCATC	3497	Db	4518	GGGGTTGGCGCGCTCGGCGCGCAGCAAGAACTTGAAGGTTGTTTTTAGAAGATCAAGATA	4577
				Qy	633	-----	633

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Db 4578 TGTTCGGATTAACGGAAGCGACCTAGCGTACGGGCGCAACAGCGCGTGGGCACCGCCGAAA 4637
Qy 634 -----Ser 634
Db 4638 TCTGGTTGTCTTCGATGTATACCTGATCCAACTCTTGTTCGGTTTCTCCAATGGCAGC 4697
Qy 635 SerPheTyrMetAlaArgAlaGlySerGlyAlaLysLysAspAsn 648
Db 4698 TCCTTCTACATGGCCGCGGAAGGGCCCAAGAAGGACAAC 4739
RESULT 3
US-10-741-849-6021
; Sequence 6021, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; FILE OF INVENTION: Use
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6021
; LENGTH: 2259
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-741-849-6021
Alignment Scores:
Pred. No.: 3,81e-99 Length: 2259
Score: 891.00 Matches: 229
Percent Similarity: 46.6% Conservative: 98
Best Local Similarity: 32.7% Mismatches: 232
Query Match: 25.7% Indels: 142
DB: 8 Gaps: 21
US-10-620-914-45 (1-648) x US-10-741-849-6021 (1-2259)
Qy 51 LeuGluSerPheTyrGlyProGlnAlaAlaAlaPhe----- 62
Db 208 TTAGAGTCATCTACAGAATCAAGCTCATATTTATGATAACACTAGAGATTTTGTG 267
Qy 63 -----AlaAlaArgLeuAlaGluArgSerAsnLeu 72
Db 268 AAAGGTAGACAAGAATGCTTAGATTAGCTATTTCCCATTTTACCACAAAAGAAAGATCTT 327
Qy 73 IleTrpValAspLeuGlyGlyThrGlyGlnValAspMetMetAlaAspTyrIle 92
Db 328 ATTTGGATGTATATGGTGGGAACTGTTCCCAATATTTGAATTCATGGATTAAGT 387
Qy 93 AspLeuAlaLys----PheLysSerIleTyrValValAspLeuCysHisSerLeuCysGlu 111
Db 388 AAATATCTGAAACTTTAAAGCTGTTTATTTGTTGATCTTTCCCATCTTTGTGTGAA 447
Qy 112 ValAlaLysLysLysAlaLysGlyTrpLysAsnValGlnValGluAlaAsp 131
Db 448 GTTGCTAAGGCAAGATTTGAAGCCCATGAATGGCAAAATGTCATGATTAGTTGCTGAT 507
Qy 132 AlaCysGlnPheAlaProProGluGlyThrAlaThrLeuIleThrPheSerTyrSerLeu 151
Db 508 GCCTGTGATTACTATTGATTATGATAGTCTGCTGATTGATTCTTTCTTATTCATTG 567
Qy 152 ThrMetIleProProPheHisAsnValIleAspGlnAlaCysSerTyrLeuSerGlnAsp 171
Db 568 TCGATGATCCCAACTTTCAATGCTGCTATCGATAATGCTGTTCTTAATAGATATGAA 627
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Qy 172 GlyLeuValGlyValAlaAspPheTyrValSer-----GlyLysTyr 185
Db 628 GGTATTATTGCACTGTGGATTTTTGGTATTCAAAGCAGTGCACCTCAATCGTGTATC 687
Qy 186 Asp-----LeuProLeuArgGlnMetProTrpSerArgArgPhePheTrpArg 201
Db 688 AATACTGTTGGTGGTGGTTAAACAGGACATTTCTTGGATATTACGTAATTTTGGAGA 747
Qy 202 SerIlePheAspIleAspAsnIleAspGlyProGluArgAlaTyrLeuGluGln 221
Db 748 ATTTGGTTTGAAGCTGATAAAAGTCTTTTGGATCTTCAAGAGAACAATAATTGGAAT 807
Qy 222 LysLeuGluArgValTrpGluGlnAsnThrGln-----GlySerIleProTyr 237
Db 808 AAATTTGGTACCGTCAAAATCTTTGAATTCATACCAAGGCGCTTTGGGTAATAATC----- 861
Qy 238 ValProTrpLeuArgAlaProTyrValTrpIleGlyArgLeuProSerValGlyHis 257
Db 862 -----CCCTATTATATTGGATTGGTTGTGATAAATCAAAATCACAC 903
Qy 258 AlaLeuHisGluGlu-----ArgValGluArgProPrometPheProProThr 273
Db 904 ACCATTTTGAAGAGATTGAATTGTTAGCCACTGAATCCCTTACCTTGCTCCAACATA 963
Qy 273 ----- 273
Db 964 ACTCCAATCGTAATCAACTTGAAGATATTCCAATTTTCTAAAGGTCATGAAGCTGCTTTA 1023
Qy 273 ----- 273
Db 1024 ATCAACTTGCANAAAAAATTTACCTTACCCTCATCTACTATCAAAAGGAATATTGGAGA 1083
Qy 274 -----PheLeuTyrThr 277
Db 1084 GTCTACTATGATGAATGAATCCATTGTTAGAACAAATTTAAAAACCAATATCATTTATGCT 1143
Qy 278 GlnSerTrpGluAspProGluProAspMetGluValMetGluIleAsnProLysAspThr 297
Db 1144 TTCACTTGGGAAGATCCTCGTGAAGATCATAAACTTTTGAATTTTACCAGTGATGATACT 1203
Qy 298 ValLeuThrLeuThrSerGlyGlyCysAsnAlaLeuAsnLeu-----LeuValGlnGly 315
Db 1204 GTTTTGGCTATTACTTCAGCTGGTGATATAATTTTGTAGTTATGCTAGTTTACCAACACCA 1263
Qy 316 AlaGlyGlnValValSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLys 335
Db 1264 CCAAAAAAGATTTCATGCTGTTGATCTTAATCCATGTCAAAACCATTTATTAGAATTGAAA 1323
Qy 336 LysValAlaIleGlnGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGlyGlyVal 355
Db 1324 TTGGCTAGTTTGTAGATGCTTTCTCAAGAACAATAATTTGGTCAATTTGGTGAAGGTAAA 1383
Qy 356 HisProArgIleGluGluLeuTyrGluLysLeuAlaProPheLeuSerGlnThrSer 375
Db 1384 ATCGAAAAATTTCAATGATCTTTTGTGATGATCTTTTGGACCGCACATGCTCTTCTAATGCC 1443
Qy 376 HisAsnPheTrpSerLysArg-----LeuTrpTyrPheGlnHisGlyLeuTyrTrpGln 393
Db 1444 TTCCAATACCTGGATGGATAAAGGACCTTAAACCTTTTCTGTGTAAGGCTCTTTAT----- 1497
Qy 394 GlyGlyMetGlyLysLeuCysTrpValLeuGlnCys-----LeuAlaValValLeu 410
Db 1498 ---GATACTGGGTTTCTAGATGGCATTAAGATATTCAAGATATGTTTCCAAAGTTGTC 1554
Qy 411 GlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArg 430
Db 1555 GGGTTTGTAGTAATACGTTTGAAGAACTTTGTGCTCAACCCATCGGAAGAACAATTTGGA 1614
Qy 431 LeuTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrp 450
Db 1615 ATTTGGAATGAACATTTG-----AAACCAACT----- 1641
Qy 451 LeuPheValLysPheVal----SerLeuValLeuPheAsnLysAlaValLeuTrpPheGly 469
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Db 1642 TTAATTAATCTCTGGTGGTTCATCTGTTGGTAATCCAAATGTTTAAATGAAGACT 1701
      ||||| ||| |||||:||||: ||| |||||
Qy 470 GlyGlyValProGlyLysGlnTyrAlaLeuLeuLysAlaAspGlyIleProIleGluAsn 489
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1702 TTGGAGTCTCCAGCTAATCAAGCAGCTTTAATG-----GGACCATCTGTTATTAAA 1752
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 490 TyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHisValArgLysGlnAsnTyr 509
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1753 TATGTTGTGTACTTTGGACCCCAATCAATTAAGAGATCGATGATTTCAAAATGATAACTAT 1812
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 510 PheTyrTyrAsnCysLeuThrGlyLysPheLeuArgAspAsnCysProThrTyrLysArg 529
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1813 TTCTACTATTATGATGATGGGAGATACACCAAAAACAATTTGCCAGATTATTAACT 1872
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 530 GluAlaAlaPheAlaThrLeuLys-----SerGlyValVal 541
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1873 ACAAAAGGTTTCAACAGATTATCTAGCACTGCTGCTACTGCCAGGGATCATCTCCAATT 1932
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 542 AsnLeuThrValSerThrAsnPheMetGlu-----GluLeuLysAlaArg 558
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1933 GACAACCTTAGAATCCACACTGACACTTTAAATGAAGTGTTTGGTAGATTAAAGAAAAA 1992
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 559 ThrTyrThrLysValIleLeuMetAspHisValAspTyrLeuAsp-----MetPro 575
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1993 TCAATCACTATTGCCATTATCATGATCATATGATGATGTTGGTTGACCTTAATGTTAGAT 2052
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 576 ValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIle 595
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2053 GCTATTAAATGAATTTACT--GCTTTGAAAAAGATGCTCTTGTCCCGAGGGGTAGAGTATTA 2109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 596 TrpArgSerAlaSerLeuSerProProTyrAlaGluLeuIleGlnLysAlaGlyPhe--- 614
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2110 CTTAGATCAGCAAGTACAAAGCCTTGGTACTTTGAAAAATTCAAGAACTTGGGATTCCAA 2169
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 615 AspValArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSer 634
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2170 GAAGAGAAAATGTTGTTGTCGAACCTGTTCAAGTATAGATATAGACAGAGTTAATATGATGCC 2229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 635 Ser 635
      |||||
Db 2230 AAT 2232
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RESULT 4

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US-10-620-914-49
; Sequence 49, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-49
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Alignment Scores:

Pred. No.:	5, 71e-94	Length:	2727
Percent:	850.50	Matches:	239
Best Local Similarity:	44.4%	Conservative:	109
Query Match:	30.5%	Mismatches:	240
	24.6%	Indels:	198
DB:	7	Gaps:	23

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US-10-620-914-45 (1-648) x US-10-620-914-49 (1-2727)
Qy 19 LeuGluLysLeuLysLysLeuSerSerMetLysAspSerLeuThrValLeuArgHisMet--- 37
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 449 TTGAGGAGCTGGAGATG---GGCTTGAAAAAGACAAAGAAATGGGAAGACATGTGTAA 505
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 38 --TrpPheGlySerLysLysGlyAspHisAlaAlaArgLeuGluSerPheTyrGly 56
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 506 CCGTGGCGGGACAG-----GGA 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 57 ProGlnAlaAlaPheAlaAlaArgLeuAlaGluArgSerAsnLeuIleTrpValAsp 76
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 524 CCG-----GGACAAAGGAGGAAACCG-ATATGGGTAGAT 555
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 77 LeuGlyGlyGlyThrGlyGluAsnValAspMetMetAlaAspTyrIleAspLeuAlaLys 96
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 GTCGTTGGGGCACAGGCTGGAATATCGAACCCATGGCCAAAGTTGTCAACGCTCTCTCAA 615
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 97 ---PheLysSerIleTyrValValAspLeuCysHisSerLeuCysGluValAlaLysLys 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 TTCTTCAAGACTGTTTACCTAGTGCATTTTCGCGGTCACCTTTGTGAAGTGGCTAGGAAG 675
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 116 LysAlaLysAlaLysGlyTyrLysAsnValGlnValValGluAlaAspAlaCysGlnPhe 135
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 CGGTTTGCAGGCTGGGTGGGAGAAATGTGAGAGTTATCTGCACGGATGCTCGCAAGTTT 735
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 136 Ala-----ProProGluGlyThr----- 141
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 AGGCTTGAGGATTATGAGGATGTTGACGAAGAGAGTCTGGCTCTGGAGATTCTTCGGCT 795
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 142 -----AlaThrLeuIle 145
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 TCTTTGTCGGTTCGTTGGGGGAGACGAGCGGGGACACATCGGGAGCTGAGTTGATC 855
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 146 ThrPheSerTyrSerLeuThrMetIleProProPheHisAsnValIleAspGlnAlaCys 165
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 ACCATGCTTATAGCTTTCGATGATGCGGATATTATTTCTCGATTATCGATTGCTCGCAG 915
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 166 SerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyrValSerGlyLysTyr 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 TCTCTGTTAGCACCTCAGCGCTTGATTCGCTCGTGGACTTTTACGCCAGTCGAAAGTC 975
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 186 Asp-----LeuProLeuArgGlnMetProTyrSerArg 196
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 976 GACTTCACATTCGCACTACACGGTGGTCTTATGAACCCGACACGTTGGCTATTTCGCG 1035
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 197 ArgPhePheTrpArgSerIlePheAspIleAspAsnIleAspIleGlyProGluArgArg 216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1036 CGAAACTTCTGGCGCTCGTTCGATGCTGACAGGGTGTCTCTTGAGCCAGCTCGTCGA 1095
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 217 AlaTyrLeuGluGlnLysLeuGluArgValTrp-----GluGlnAsnThrGln 232
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1096 GATTATCTCGAGTACAGGTTTCGGGACTGCTCTGACCCGTCAACGCCGCAACACTTTG 1155
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 233 GlySerIleProTyrValProTyrLeuArgAlaPro-----TyrTyrVal--- 247
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1156 GGAGCAATCTTACTACATCTGTTGGG-ATGCTCTCAAGAAGCCCTTTTCTACGTCGAG 1214
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 248 -----TrpIleGlyArgLeuPro----- 253
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1215 TCTACCACACGAAATTTGTGGAACACATCGATGCTATTTCGACAGAGTCCCCAAGATCATC 1274
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 253 ----- 253
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1275 ACCCGCTCTAGTGGGCAAAACATTTCTTCTCAGCAACAAATGCGCTTAGCTTTGCGAGTCGG 1334
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 254 -----SerValGlyHisAlaLeu-----HisGluGluArgValGlu 265
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1335 CCGCACACGCGCGGAGATGCGCTCAAGGCCCTTCAATACGGCCATCGAGACATCTCGGC 1394
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 266 ArgPro-ProMet----- 269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1395 CAACCTACCTCTCCCGTCTCTTCTTCTACAAAAATCACCATCGAGGATCTACTACGACGA 1454
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 270 -----PheProThrPheLeuTyThrGlnSerTrpGluAs 282
Db 1455 TCAACTCCCGAAGCACACCAGTTCAATGACGAGTACATCTACGCGTTTACCTCGGAAGA 1514
QY 282 pProGluProAspMetGluValMetGluLeuLeuAsnProLysAspThrValLeuTh 302
Db 1515 CTCGGCGTGCAGACAGAACTCTTAACCTCGGGCCGACGCTGCTAGCCATCAC 1574
QY 302 rSerGlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValValSerVa 322
Db 1575 CAGCGCGGCGACAACATCTTCTTACCTGATGACGAGTCCGCGTCCGCTGACGCCAT 1634
QY 322 lAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaGlnGlnLe 342
Db 1635 CGACCTAAACCCAGCCCAACACCTGCTTGAACCTCAAAAGTCGCGCTCTTTTACGACTCT 1694
QY 342 ucluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgGlieGluGlu 362
Db 1695 GGAATTACCCGACGCTGTGAAGATCTTCGGTGAGGGCAACACACCCGACTTTTCGCTCACT 1754
QY 362 uTyrgLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysAr 382
Db 1755 GCTCATCTCCAACTCTCCCTCACCTTCGCGCGCGGTTTCAATACTGCTATCCAA 1814
QY 382 gLeuTrpTyThrPheGln-----HisGlyLeuTyThrGlnGlyGlyMetGlyLy 398
Db 1815 TCGGCACATATTATCCGACCTCGCGGGCGGCTCTCTATGATACCGCGGCTCCCGATA 1874
QY 398 sLeuCysTrpValLeuGlnCysLeuAlaValValLeuGlyLeuGlyLysThrValLysAr 418
Db 1875 CGCTATCGCTTTCCTCCGCTGATTTCCACACTCTTCTTCTGCGCTCCGCGCTCCGTCG 1934
QY 418 gLeuAlaAsnAlaProThrMetGluGlnArgArgLeuTrpAspSerAsnMetLeuI 438
Db 1935 ACTTCTCTACTCTCCACCTCGAAGGCAAGTTCCTATCTACACACCAAGATT----- 1989
QY 438 eHisPheValLysAsnGlyProLeuValTrpLeuPheValLysPheValSer-- 457
Db 1990 -----CGTCCCTGT-----CTGCTCAACCGCTTCTGTCACCGG 2021
QY 458 -leuValLeuPheAsnLysAlaValTrpPheGlyGlyValProGlyLysGlnTy 477
Db 2022 CTTGTCTCTCAGCTCCGACGCTTCTCTGTGCGGCTTTGGCGTGGCCCAAGATCAAGT 2081
QY 477 rAlaLeuileLysAlaAsp----- 483
Db 2082 GGCTATGATCGAAGCGGACTACACCGCGGTCTATCTCTCTCCACCCACCCCGAGCAG 2141
QY 484 -----GlyIleProileGluAsnTyThrIleAlaArgThrMetAspGl 497
Db 2142 CAAGAAAAAACCAAGCCGCGCGGAAGCAATCTCCACTACACAACCTCCACCTTGATCC 2201
QY 497 yValAlaGluAsnSerHisValArgLysGlnAsnTyThrPheTyThrAsnCysLeuThGl 517
Db 2202 CGTCTCTCCACCTCCCACTTCGCTCGGCAACACCTTACTACTCTGCTGTGCTCGG 2261
QY 517 yLysPheLeuArgAspAsnCysProThrTyThrArgGluAlaAlaPheAlaThrLeuLy 537
Db 2262 ACAATACACGCCAGTGCATCCCGATTACTTTCCCTCGCGCCCACTCTACTACTCAG 2321
QY 537 sSer---GlyValValAspAsnLeuThrValSerThrAsnPheMetGluGluLeu-- 555
Db 2322 CGCTCCTGGAGCCTTGACGGCTTACCGCATCCACAGGATGAATAACAGGAGGTGTTGGC 2381
QY 556 -----LysAlaArgThrTyThrLysValIleLeuMetAspHisValAspTrpLeuAs 573
Db 2382 TAGGTTTCAGCGGGGTACTTTGACAGTAGCGGTGGTGATGATAGTAGTGGATTGTTTCCA 2441
QY 573 pMetPro-----ValAlaAsnGluLeuAlaGluCy 583
Db 2442 TCCGCTTTCGCTGAGGAGGAAAGAAAGGAGGCGAAGCGGAGGAGCAAGTGGAGG 2501
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QY 593 sLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAlaSerLeuSerPr 603
Db 2502 GTTGAATCGGCGTTCGAAGGTGCGAAGGTGTGTTGTTGAGGAGCGCGGAGTGGAGCC 2561
QY 603 oProTyrrAlaGluLeuIleGlnLysAlaGlyPheAspValArgCysIle----- 619
Db 2562 GTGGTATGTGAGGGTTTTGTGAGGAAGGGTTTGAGCAAGAGGGTGGGTGTCGTGA 2621
QY 620 ----ArgArgAlaThrGlnGlyTyThrMetAspArgValAsnMetTyThrSerPheTyMe 638
Db 2622 ATCCGGAAGGGGGGACAGGAGTGTATTGACAGGGTGAATATGTATGCTAGTTGTTGGAT 2681
QY 638 tAlaArgArg 641
Db 2682 CTTGGAAGAAG 2691
RESULT 5
US-10-620-914-48
; Sequence 48, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 48
; LENGTH: 3427
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-48
Alignment Scores:
Pred. No.: 5,11e-88 Length: 3427
Score: 804.00 Matches: 238
Percent Similarity: 43.2% Conservative: 112
Best Local Similarity: 29.4% Mismatches: 256
Query Match: 23.2% Indels: 205
DB: 7 Gaps: 24
US-10-620-914-45 (1-648) x US-10-620-914-48 (1-3427)
QY 19 LeuGluLysLysLysLeuSerSerMetLysAspLeuThrValLeuArgHisMet--- 37
Db 776 TTGGAGGAGCTGGAGATG---GGCTTGAATAAAGACAAAGGAATGGGAAGACATGTGTA 832
QY 38 ---TrpPheGlySerLysLysGlyAspHisAlaAlaArgLeuGluSerPheTyGly 56
Db 833 CCGTGGCGCGGACAGGACCGGGACAAGGA-----GGAACCGATATGG 877
QY 57 ProGlnAlaAlaPheAlaArgLeuAla-----GluArgSerAsn 71
Db 878 TAGATGATGCGCTCTCATCAGAACCTTGCATGTTGAAATCCACACAGCGTGACC 937
QY 72 LeuIleTrpValAspLeuGlyGlyGlyThrGlyGluAsnValAspMetMetAlaAspTy 91
Db 938 ATCGCTACAAAACAGGTCGGTGGGGCACAGGCTGGAATATCGAAGCATATGCCCAAGTTT 997
QY 92 IleAspLeuAlaLys---PheLysSerIleTyThrValValAspLeuCysHisSerLeuCy 110
Db 998 GTCACGCTCTGTAATCTTCAAGACTGTTTACCTAGTGGACTTTTCGCCGCTCACTTGT 1057
QY 111 GluValAlaLysLysAlaLysAlaLysGlyTyThrLysAsnValGlnValGluAla 130
Db 1058 GAAGTGGCTAGGAAGCGGTTTCCAGCGTGGGGAGAGATGTGAGAGTTATTCGACG 1117
QY 131 AspAlaCysGlnPheAla-----ProProGluGlyThr----- 141
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US-10-620-914-45 (1-648) x US-10-620-914-1 (1-1252)
Qy 231 ThrGlnGlySerIleProTyrValProTrpLeuArgAlaProTyrTyrValTrpIleGly 250
Db 4 ACGCAGTTGCGCCCTCACCGACCTGCCC-----GCCCGCGC-----GTTGCC 45
Qy 251 ArgLeuProSerValGlyHisAlaLeuHis-----GluGluArg 263
Db 46 CGC-----CAGATCGGCGCGCGCTGCACCGCAGCTCGCTTCAGCGCCGAGAGCATG 99
Qy 264 ValGluArgProProMetPheProThrPhe-----LeuTyrThrGlnSerTrp 280
Db 100 ATGAGAGCG-----ATGTTCTCGCGCTCTTCACGGCCCTCGTATATCCGACATCTGG 153
Qy 281 GluAspProGluProAspMetGluValMetGluLeuAsnProLysAspThrValLeuThr 300
Db 154 GAGGATCGGCGGTGGACATCGCGGCCCTCGCCATCCGCCCGCGGGACCGGTGTGGCC 213
Qy 301 LeuThrSerGlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVal 320
Db 214 ATCGCCTCGGCGGTGCAACGTGCTTCTCTATCTACGACGAGGGCGCGGCTCGATCCTC 273
Qy 321 SerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGln 340
Db 274 GCCGTGATCTCTCGCCGCCCATGTGGGGCTGGGGCGGCTGAAGCTCGCCGCCGCGGG 333
Qy 341 GlnLeu-----GluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIle 359
Db 334 ACGCTCGCCGACCATCGCGCTTCTTCGATCTCTTCGGTCGCGCAGACCTCGCCGGCAAT 393
Qy 360 GluGluLeuTyrGluLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrp 379
Db 394 CGCGCCCTCTACGACCGCCCATCGCGCCCGCTCGACGGCGGAGCGCGCTACTACGG 453
Qy 380 -----SerLysArgLeuTrpTyrPheGlnHisGlyLeuTyrTrpGln 393
Db 454 GAGGCGCGCAGCCCTTCGCGCGCGGCATCCAGCTGTTTCGAGCGCGCTTACCGGCAC 513
Qy 394 GlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLeuAlaValValLeuGlyLeuGly 413
Db 514 GGTGCGCTTCGCGCGCTTTCATCGCGCGGCCCATACGCTCGCG-----CGGCGCGCGGCG 567
Qy 414 LysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLeuTrpAsp 433
Db 568 ACCGACCTCGCGGGCTTCTCGACTGTCCGACATCGAGCGCGCGCTTCTTCTAC 627
Qy 434 SerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLeuPheVal 453
Db 628 GCCCATATC-----GGGCG-----CTCTTCGAG 651
Qy 454 LysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyValPro 473
Db 652 GCGCGCGGTGTGCAGCGCGCTCGCCGACGCGCGCGCGCTTTCGCGGTGGGATCCCG 711
Qy 474 GlyLysGlnTyrAlaLeuIleLysAlaAspGly-----IleProIleGluAsn 489
Db 712 CCCGCGCAATATGCGCTTCTGGCGGGAGACGGCGACCGCGAGCTGCTGCCGCTG----- 765
Qy 490 TyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHis----- 503
Db 766 -----CTGCGCGCAGCGCTCCACCGGCTGCTGTGACTTC 801
Qy 504 ValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeuArgAspAsn 523
Db 802 CCCCTGCGCGAAGACTACTTCTGCGCTTCAGGCGCATCGCCCGCGCTATCCGCGCGCGCG 861
Qy 524 -----CysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyVal 540
Db 862 GAGGCGCGCTGCGCCCTTCTCGAACCCCGCTTTCGAGACCGCTGCGGAGAAC----- 918
Qy 541 ValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLysAlaArgThrTyr 560
Db 541 ValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLysAlaArgThrTyr 560
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Db 919 GCGGCGCGGTGCAGATCGAGAACCGCAGCTGTACCGAGGCGCTCGCGCGGAACCCGAG 978
Qy 561 ThrLysVal-----IleLeuMetAspHisValAspTrpLeuAspMetProValala 577
Db 979 GAGAGCATCCAGCGCTTACCTCTGCTCGATCGCAGGACTGGATGACCGAGCGGAGCTG 1038
Qy 578 AsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArg 597
Db 1039 ACCGCGCTCTCGCGCGCAGGTGACGGCACTGACGGCGCGCGCGGGTGTATCTTCGC 1098
Qy 598 -----SerAlaSerLeuSerProProTyrAlaGluLeuIleGlnLysAlaGlyPhe 614
Db 1099 ACCGCGCGGCGCGCGACCTGTCTGCC-----GGCCGAGTCCCGGAGAGATCTCCGG 1152
Qy 615 AspValArgCysIleArgArgAlaThrGlnGly-----TyrMetAspArgValAsnMet 632
Db 1153 CACTGGCGCGCGCGACCGGGCGCGGACAGCGCGGCGCATCGCGCGGCGATCGCGCGATC 1212
Qy 633 TyrSerSerPheTyrMetAlaArgArgLysGlyAla 644
Db 1213 TACGGCGCTTCCACTCTACGGCGGAGGACGCC 1248

RESULT 8
US-10-118-495-22
; Sequence 22, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-118-495-22

Alignment Scores:
Pred. No.: 1,398-29 Length: 1248
Score: 329.00 Matches: 118
Percent Similarity: 42.8% Conservative: 66
Best Local Similarity: 27.4% Mismatches: 184
Query Match: 9.5% Indels: 63
DB: 5 Gaps: 15

US-10-620-914-45 (1-648) x US-10-118-495-22 (1-1248)
Qy 248 TrpIleGlyArgLeuProSer-----ValGlyHisAlaLeuHisGluGluArgValGlu 265
Db 48 TGGAAAGCCGCTTACACAGAACCGCGCTTTCCAAAGCGGCATCTCCGAGCGGCTGT 107
Qy 266 ArgProProMetPheProPro-ThrPheLeuTyrThrGlnSerTrpGluAspProGluPr 285
Db 108 GCGCTTCTGTTTTCGCGCTCTGTC-----TATCCGAGATCTCGGAAGACCCCGATG 161
Qy 285 OAspMetGluValMetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyGln 305
Db 162 CGACATGAGCGCATGACGTGTTGTCAGGCGCATCGCATCTGCACATCGTTCGCGCGG 221
Qy 305 yCysAsnAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValValSerValAspCysAs 325
Db 222 CTGCAACATCTCTGCGCTACCTCACCGTTCGCGCGCAGGATCGACGCGCTCGACTCAA 281
Qy 325 nProIleGlnSerAlaLeuLeuLysLysValAlaIleGlnGlnLeuGluPheGln 345
Db 282 CGCGCGCCCATCGCGCTGAACCCGATGAAGCTGGAGCGGTGCGCGCTGCTCCCTCGCA 341
```

Qy 345 u---AspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrG1 364
Db : |||:||||:|||||
342 GGGCGATGTTCCGCTTTTCGGCGCGCCGACACACCGCCATTCGCAAGCCTATGA 401
Qy 364 uLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTr 384
Db : |||:||||:|||||
402 CCGCTTTATGCGCGCATCTCGATCCGTCAGCCGACCATATTCGGAGCGCCGCAACTG 461
Qy 384 p-----TyrPheGlnHisGlyLeuTyrTrpGlnGlyGlyMetG1 397
Db : |||:||||:|||||
462 GCGTGTGCGCGCGCATCGCGCTCTTCAGCGCAATTTCTACACGACCGCGCTCTCGG 521
Qy 397 YLysLeuCysTrpValLeuGlnCysLeuAlaValValLeuGly----- 411
Db : |||:||||:|||||
522 C-----CTGTTTCATCGCATGGCGCCATCGCAGCGCGCAAAATT 557
Qy 412 -LeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLe 431
Db : |||:||||:|||||
558 CTTCCGCGTCAACCGCGCCCATATGGAAGCCAGGAATATCGCGAGCGCGCTT 617
Qy 431 uTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLe 451
Db : |||:||||:|||||
618 CTTCAACGAGGAGCTGGCGCGCTCTTCGACAG-----AAGCTTTTGAATGGCG 668
Qy 451 uPheValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGly 471
Db : |||:||||:|||||
669 GACCTCGGTAAGGCGCTCGCTG-----TTCCGCGCTCGG 701
Qy 471 yValProGlyLysGlnTyr-----AlaLeuIleLysAlaAspGlyIleProIleGluAs 489
Db : |||:||||:|||||
702 CATTCCGCGCGCGAGTACGATCCCTGATCAGCTCAGCGAGCGACCATGGCGAGCGT 761
Qy 489 nTyrIleAlaArg-----ThrMetAspGlyValAlaGluAsnSerHisValAr 505
Db : |||:||||:|||||
762 TCTGAAGCGCGCTGGAAAGCTCGCTCGATTTCCCTGGAAAC----- 810
Qy 505 gLysGlnAsnTyrPheTyrTrpAsnCysLeuThrGlyLysPheLeuArgAspAsn----- 523
Db : |||:||||:|||||
811 -----AATTATTTCGCTCGAGGCTTTTCGCGCGCGCTATCCAAATCCCGTGAGGC 863
Qy 524 ---CysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyValValAs 542
Db : |||:||||:|||||
864 CGCCCTGCGCGCTATCTGGAAGAGAGAACTAGCAAAACCATCCGC---GGCAATATCGA 920
Qy 542 pAsnLeuThrValSerThrAsnPhePheMetGluGluLeu-----LysAlaArgTh 559
Db : |||:||||:|||||
921 CCGGTGCGCATCCACCATGCAATCTGATCGAATTCCTCGCGCAGGAGCGGGCAC 980
Qy 559 rTyrThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProValAlaAsnG1 579
Db : |||:||||:|||||
981 CGTCGATCGCTTCATCTGCTCGATCGCAGGACTGGATGACCGATGACCAAGCTCAACGC 1040
Qy 579 uLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAl 599
Db : |||:||||:|||||
1041 GCTGTGTGCGAAATCCAGCCACCGCTCCGCGAGCGCGCGCTCATCTTCGCGACCGC 1100
Qy 599 a-----SerLeuSerProTyrAlaGluLeuIleGlnLysAlaGlyPheAsp-V 616
Db : |||:||||:|||||
1101 CGCGAGCCGAGCTGTGCGCAGCGCGGTCTCGACCTCGCTGCTCGACCACTGGGACTA 1160
Qy 616 alArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSerSerP 636
Db : |||:||||:|||||
1161 TCAGGACGAGGCGTTCGCGCAATCTTCGCGACGC-GACCGTTCGCGCATCTATGCGCGCT 1219
Qy 636 heTyrMetAlaArgLysGlyAla 644
Db : |||:||||:|||||
1220 TCCACCTCTATGTGAAGCGCACGGCA 1245

RESULT 9

US-10-620-914-22

; Sequence 22, Application US/10620914

; Publication No. US20040093639A1

GENERAL INFORMATION:

; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; PRIOR FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-620-914-22

Alignment Scores:

Pred. No.: 1,39e-29 Length: 1248
Score: 329.00 Matches: 118
Percent Similarity: 42.8% Conservative: 66
Best Local Similarity: 27.4% Mismatches: 184
Query Match: 9.5% Indels: 63
DB: 7 Gaps: 15

US-10-620-914-45 (1-648) x US-10-620-914-22 (1-1248)

Qy 248 TrpIleGlyArgLeuProSer-----ValGlyHisAlaLeuHisGluGluArgValGlu 265
Db : |||:||||:|||||
48 TGGAAAGCGCGCTTACCAAGACCGCGGCTTTCCAAAGCCGCGATCTCCGAGCGGCTTT 107
Qy 266 ArgProMetPheProPro-ThrPheLeuTyrThrGlnSerTrpGluAspProGluPr 285
Db : |||:||||:|||||
108 GCGCTTCTCTGTTTTCGCGCTCGTC-----TATCGCAGATCTGGGAAGACCCGATGT 161
Qy 285 oAspMetGluValMetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyG1 305
Db : |||:||||:|||||
162 CGACATGGAGGCCATGCGACTTGTGTAGGCGCATCGCATCTGTCACAAATCGCTTCGCGCG 221
Qy 305 yCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValValSerValAspCysAs 325
Db : |||:||||:|||||
222 CTGCAACATCTCGCTTACCTACCTCCGCGCGCGGATCGACGCGCTCGACCTCAA 281
Qy 325 nProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleGlnGlnLeuGluPheG1 345
Db : |||:||||:|||||
282 CGCGCGCCACATCGCGCTGAACCGCATGAGCTGAGCGGTGCGCGCTCTGCCCTCGCA 341
Qy 345 u---AspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrG1 364
Db : |||:||||:|||||
342 GGGCGATCTGTTCGCGCTTTTCGCGCGCGCCAGCCACCAATTCGCAAGCCTATGA 401
Qy 364 uLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTr 384
Db : |||:||||:|||||
402 CCGCTTTATGCGCGCATCTCGATCCGTCAGCGCGCGCCATTCGCGAGCGCGCAACTG 461
Qy 384 p-----TyrPheGlnHisGlyLeuTyrTrpGlnGlyGlyMetG1 397
Db : |||:||||:|||||
462 GCGTGTGCGCGCGCATCGCGCTTTCGCGCGCAATTTCTACACGACCGCGCTCTCGG 521
Qy 397 YLysLeuCysTrpValLeuGlnCysLeuAlaValValLeuGly----- 411
Db : |||:||||:|||||
522 C-----CTGTTTCATCGCATGGCGCCATCGCAGCGCGCAAAATT 557
Qy 412 -LeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLe 431
Db : |||:||||:|||||
558 CTTCCGCGTCAACCGCGCCCATATGGAAGCCAGGAATATCGCGAGCGCGCTT 617
Qy 431 uTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLe 451
Db : |||:||||:|||||
618 CTTCAACGAGGAGCTGGCGCGCTCTTCGACAG-----AAGCTTTTGAATGGCG 668
Qy 451 uPheValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGly 471

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Db 669 GACCTCGGTAAAGCCTCGCTG-----TTTCGGCCTCGG 701
Qy 471 yValProGlyLysGlnTyr-----AlaLeuIleLysAlaAspGlyIleProIleGluAs 489
Db 702 CATTCGGCGCGGAGTACGATTCCCTGATCACCTCAGCGACGCGACCATGGCAGCGT 761
Qy 489 nTyIleAlaArg-----ThrMetAspGlyValAlaGluAanSerHisValar 505
Db 762 TCTGAAGCCCGCGGTGGAAAGCTCGCTCGCATTTTCCCTCGGAAAC----- 810
Qy 505 gLysGlnAsnTyRPhTyTyrAsnCysLeuThrGlyLysLeuArgAspAsn----- 523
Db 811 -----AATTATTTCGCTGGCAGGCTTTTCCCGCGCGCTATCCAAATCCCGGTGAGGC 863
Qy 524 ----CysProThrTyRLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyValValas 542
Db 864 CGCCTGCGCGCTATCTCGAAAGACAGAACTACGAAACCATCCGC---GGCAATATCGA 920
Qy 542 pAsnLeuThrValSerThrAsnPhePheMetGluGluLeu-----LysAlaArgTh 559
Db 921 CCGCGTGCCTATCCACCATGCCAATCTGATCGAATTCCTCGCGGCAAGGACGCGGGCAC 980
Qy 559 rTyThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProValAlaAsnGl 579
Db 981 CGTCGATCGCTTCATCTGCTGCTGATCGCAGAGACTGGATGACCGATGACCATCGC 1040
Qy 579 uLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAl 599
Db 1041 GCTGTGTGCGAAATCAGCCGACCGCTCCGCGAGCGCGCGCTCATCTTCCGACCGC 1100
Qy 599 a-----SerLeuSerProProTyRAlaGluLeuIleGlnLysAlaGlyPheAsp-V 616
Db 1101 CGCGAGCCCGAGCTGTGCGCAGGCGCGTCTCGACCTCGCTGCTCGACCATGGGACTA 1160
Qy 616 alArgCysIleArgArgAlaThrGlnGlyTyRMetAspArgValAsnMetTyRSerSerp 636
Db 1161 TCAGGACGAGCGTTCGCGGAAATCTCGGCACGC-GACCGTTCGGCCATCTATGGCGCT 1219

RESULT 10
US-10-118-495-28
; Sequence 28, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-118-495-28

Alignment Scores:
Pred. No.: 2,86e-29 Length: 1251
Score: 326.50 Matches: 115
Percent Similarity: 47.6% Conservative: 71
Best Local Similarity: 29.4% Mismatches: 162
Query Match: 9.4% Indels: 46
DB: 5 Gaps: 14
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US-10-620-914-45 (1-648) x US-10-118-495-28 (1-1251)
Qy 275 LeuTyRThrGlnSerTrpGluAspProGluProAspMetGluValMetGluIleAsnPro 294
Db 130 GTCTATCCGAGATCTGGGAAGACCCGAGATCCACATGGAGATGGAGCTTGGCGAA 189
Qy 295 LysAspThrValLeuThrSerGlyGlyCysAsnAlaLeuAsnLeuValGln 314
Db 190 GGCACCGCATCTGCACATCGGCTCGGCGGCTGCAACATGCTGGCTATCTCTCGCGC 249
Qy 315 GlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAlaLeuGluLeu 334
Db 250 AACCGCGCCAGCATCGATGTGTGGACCTCAACCGCACCATCGCGCTCAACAAGCTG 309
Qy 335 LysLysValAlaIleGlnGlnLeu---GluPheGluAspValTrpGlnLeuPheGlyGlu 353
Db 310 AAGCTCGCTGCTTCCCGCATCTCCCGCCCATCAGGATGTGGTGGCCATCTCGCGCGC 369
Qy 354 GlyValHisProArgIleGluGluLeu-TyrGluLysLysLeuAlaProPheLeuSerGl 373
Db 370 GCCCG-CACCGCGACACAGCGTCGGTTATGACCGTTTCATCGCGAGCATCTGGATGC 428
Qy 373 nThrSerHisAsnPheTrpSerLys-----ArgLeuTyRTrpPh 386
Db 429 CACGACCAAGGCATACTGTCGAAGCGCACCCCTTTCCGGCGCGCTTCGCTTCGGTGT 488
Qy 386 eGlnHisGlyLeuTyRTrpGlnGlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLe 406
Db 489 CGACAGGAACATCTACCGGACCGCTCTCGCGCGTTTCATCGGCGCGCGGCACATCAT 548
Qy 406 uAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGl 426
Db 549 GCCCGCTGACCGCGTGAACTCACC-----GAAATGCCAACACCCGCGCTCGGA 602
Qy 426 uGluGlnArgArgLeuTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLy 446
Db 603 CGAACAGCGCCAGTTTTTGACGAAGGTCGCGCGCTTTTC-----GACAA 650
Qy 446 sProLeuVal---TrpLeuPheValLysPheValSerLeuValLeuPheAsnLysAlaVa 465
Db 651 GCCGCTGTGTGCTGTGGCTGACGAAGCGCAAGCTCGCTT----- 690
Qy 465 lLeuTrpPheGlyGlyValProGlyLysGlnTyr-----AlaLeuIleLysAl 482
Db 691 -----TTCCGCTTGGCATTCGCGCGCGCAGTATGACGAGCTGGCAAGCTTTCCAG 743
Qy 482 aAspGlyIleProIleGluAsnTyRlleAlaArgThrMetAspGlyValAlaGluAsnSe 502
Db 744 CGACGCGC---ACGGTTGCTCTCCCTCCTCAAGGAGCGGCTGGAAAGCTTGGCTGCAACT 800
Qy 502 rHisValArgLysGlnAsnTyRPhTyTyrAsnCysLeuThrGlyLysPheLeuArgAs 522
Db 801 CCCGCTC---AGCGACAAATATTTCGCTGCGAGCGCTTTCGGCGCGCTTATCCCGAGCC 857
Qy 522 pAsn-----CysProThrTyRLeuArgGluAlaAlaPheAlaThrLeuLysSerGl 539
Db 858 GCATGAGGTCCTCGCGCTTATCTCAACCGGAATATTACGAAAGATCGCAACA 917
Qy 539 yValValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLys----- 556
Db 918 CACCGCG---CGCGTTCGCGGTGCATCAGCCACCTATACCGAGCTGCTTTCCCGCAAGCC 974
Qy 557 -AlaArgThrTyRThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProVa 576
Db 975 GGCAATGGCGTCGACCGCTATATCTCTCGATCGCGAGCTGGATGACGGATGTGCA 1034
Qy 576 lAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTr 596
Db 1035 GCTCAACGAGTTATGGTCGACATCAGCGCGCATCCCGCGGACGCGCTCATCTT 1094
Qy 596 pArgSerAlaSerLeu-----SerProTyRAlaGluLeuIleGlnLy 611
Db 1095 CCGCACCGCGCGCGA-AAAGAGCGTTATCGAGGCGCGCTTTTCGCGCGGACATCCGCAACC 1153
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Qy 373 GlnThrSerHisAsnPheTrpSer-----LysArgLeuTrpTyr 385
Db 430 CCGCAACCCGCGCTATTGGAACGGCGAGATCTCACGGCGCGCGCGCATCGCGCTC 489
Qy 386 PheGlnHisGlyLeuTyrGlnGlyGlyMetGlyLysLeuCysTyrValLeuGlnCys 405
Db 490 TTCGGCGCCACAGTITATCGTACCGCGCTGCTTGGCGGTTCATTTCGCCCGCAGCATGCT 549
Qy 406 LeuAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMet 425
Db 550 CTCGCACGGCTGCACGGCATCAATCCG-----GAAGATTTTCGCAAGCGCGCTCCATG 603
Qy 426 GluGlnGlnArgArgLeuTrpAspSerAsnMetLeuLeHisPheValLysAsnGlyPro 445
Db 604 CGCAGCAGCAGCGAGCTTCTCGACGACAGCTCGCTCGCTCTTC-----GAG 651
Qy 446 LysProLeuVal--TrpLeuPheValLysPheValSerLeuValLeuPheAsnLysAla 464
Db 652 GTCGCGGTATCCGTTGGATCACAGCCGCAAGAGCTCCCTT----- 693
Qy 465 ValLeuTrpPheGlyGlyValProGlyLysGlnTyrAlaLeuLeLysAlaAspGly 484
Db 694 -----TTCGGCTCGGCATCCCGCGCAGCAGTTTCGACGAACTCGCGAGC----- 738
Qy 485 IleProIleGluAsnTyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHisVal 504
Db 739 CTGAGCCGGAGAAATCCGTCGCGCGTGTCTGCGCAATCCCTGGAAAGCTGACCTGT 798
Qy 505 Arg-----LysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeuArg 521
Db 799 CATTTCCCTTTCGCGGTAATACTTACTTCGCTCGCGAGGCTTTTCGACGGCGCTACCGCGG 858
Qy 522 AspAsn-----CysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSer 538
Db 859 CCGACAGGGCGAGTTCGCCACCTTATCTTACGGCATCGCATACGAGCGATTTCGGCAG 918
Qy 539 GlyValValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeu----- 555
Db 919 AAT---GGGAGCGCGTCGAGTCCACCATCGAGCTTTCAGGAGCTTTCGCGCGCAAG 975
Qy 556 LysAlaArgThrTyrThrLysValIleLeuMetAspHisValAspTyrTrpLeuAspMetPro 575
Db 976 CCCCGCGCTCAGTCGACCGCTAGTGTCTCTCGACGACAGGACTGTGATACCGACGAG 1035
Qy 576 ValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIle 595
Db 1036 CAGCTGAACGACCTTCGACCGAGATCACCGCACCGCGCGCGCGCGCTCGTGATC 1095
Qy 596 TrpArgSer-----AlaSerLeuSerProPro-----TyrAlaGluLeuIleGln 610
Db 1096 TTCGCACGGCGCGCGAAGCGAGCATCTCGCGGGCGCTCTCCACCACCTCTCTCGAT 1155
Qy 611 LysAlaGlyPheAspValArgCysIleArgAlaThrGlnGlyTyrMetAspArgVal 630
Db 1156 CAGTGTACTATGATGCGCAGACTTCGATGAGGCTC-----GGCGCTGAAGACCGGTG 1209
Qy 631 AsnMetTyrSerSerPheTyrMetAlaArgArgLys 642
Db 1210 CGGATCTATGCGCGCTTCCACATCTACCGGAAGAAA 1245
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RESULT 14

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US-10-085-959-12
; Sequence 12, Application US/10085959
; Publication No. US20030165870A1
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Welch, Rodney A.
; APPLICANT: Burland, Valerie D.
; TITLE OF INVENTION: No. US20030165870A1el Sequence of E. Coli CFT073
; FILE REFERENCE: 960296.97648
; CURRENT APPLICATION NUMBER: US/10/085,959
; CURRENT FILING DATE: 2002-03-01
```

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; PRIOR APPLICATION NUMBER: 60/242,412
```

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; PRIOR FILING DATE: 2000-10-19
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; NUMBER OF SEQ ID NOS: 255
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; SOFTWARE: PatentIn version 3.11
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; SEQ ID NO 12
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; LENGTH: 4246
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; TYPE: DNA
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; ORGANISM: Escherichia coli
```

```
US-10-085-959-12
```

Alignment Scores:

Pred. No.:	0.00109	Length:	4246
Score:	128.00	Matches:	139
Percent Similarity:	34.1%	Conservative:	108
Best Local Similarity:	19.2%	Mismatches:	207
Query Match:	3.7%	Indels:	272
DB:	6	Gaps:	40

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US-10-620-914-45 (1-648) x US-10-085-959-12 (1-4246)
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Qy 24 LeuSerSerMetLysAspAspLeuThrValLeuArgHisMetTrp-PheGlySerLysLy 43
Db 2393 ATTCAACAGGCTAGGGAGGATATCCGTATCTCGCCCACTGCAGTTTCTGCAACAAAC 2452
Qy 43 sGlyAspAspHisAlaAlaArgLeuGluSerPheTyrGlyPro-----G1 58
Db 2453 CGGTGAGTCTCACTCA-----CCATACTTTCATCCACTGACGCCAGCCTGAAC 2500
Qy 58 nAlaAlaAlaPheAlaAlaArgLeuAlaGluArgSerAsnLeuIleTrp----- 74
Db 2501 AGGCTGGGTTTTTCATG---TGCACAGAAAACCCCGAGCTAGCTGGGGTTCCGGAA 2557
Qy 75 -----ValAspLeu----- 77
Db 2558 AGCTTTCAGCTTTGAGCGCGATTATTAACCCCTTTGATTGTTTAAACACTTTTGGCGT 2617
Qy 78 -----GlyGlyGlyThrGlyGluAsnValas 86
Db 2618 CTGCAACTGCAAGTGTCAACAAAGAAATCAAAAGGGGGTCCCAATGGGGAACGAAAGA 2677
Qy 86 pMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIleTyrValValAspLeuCy 106
Db 2678 GCTTAGCGCACACCCGATGGNACTG-----TAAATATC 2710
Qy 106 sHisSerLeuCysGlu-----ValAlaLysLysLysAla-LysAlaL 120
Db 2711 ACATAGTTTTTGGCCCAAAATACCGAAGACAGAGGTGTTCTACAGAGAGAAGCGTAGACAA 2770
Qy 120 ySGly-----TrpLysAsnValGlnValValGluAlaAspA 132
Db 2771 TAGGCAGTATTTTGAGAAAGCTGTGTGAGTGGAAAGCGTACGGATTCTGGAAGCTGAAT 2830
Qy 132 laCysGlnPheAlaProGluGlyThrAlaThrLeuIleThrPheSerTyrSerLeu 152
Db 2831 GCTGT-----GCNATCATATCATATGCTTGT 2857
Qy 152 hrMetIleProProPheHisAsnValIleAspGlnAlaCysSerTyrLeuSerGlnAspG 172
Db 2858 TGGAGATCCCGCCC-----AAAATGAGCGGTATCCG 2887
Qy 172 lyLeuValGlyValAlaAspPheTyrValSerGlyLysTyrAspLeuProLeuArgGln- 191
Db 2888 GGTTTATGGGA-----TATCTGAAGGGAAGCAGTCTGTGTTTACGAGC 2935
Qy 192 -----MetProTrpSerArgArgPhePheTrpArgSerIlePheAspI 206
Db 2936 AGTTTGTGATTTGAAATTCAAATACAGGAACAGGGAGTTCTGTGTCAGAGGCTACTACG 2995
Qy 206 leAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGlnGlnLysLeuGluArgV 226
Db 2996 TCGATACAGTGGT-----NAGAACCGCGCGAAGATACAGGATTACATAAGCACC 3046
Qy 226 alTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrTrpLeuArgAlaProTyr- 245
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Db 3047 AGCTGAAGAGATAAATGGGAGAGCAGTATCATCCATCCCTATCCGGCAGCCCGTTA 3106
      |||:||||: ||| :|||:||||: :|||:||||:
Qy 246 -----TyrValTrpIle-----GlyArgLeuProSerValGlyHisA 258
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3107 CGGCGCGTAAGTAACGAAGTTGGATGCAAAATGTGAGTGTGCGCTGTAGGCGCG 3166
      |||:||||: |||:||||: |||:||||: |||:||||:
Qy 258 laLeuHisGluGluArgVal-----GluArgProProMetPhePro-ThrPhe 274
      |||:||||: |||:||||: |||:||||: |||:||||:
Db 3167 GCTGTAAGAGAGCGCTTATAGCGCATTTTGAACCACTCCGGCTATGCCGAGAGATATT 3226
      |||:||||: |||:||||: |||:||||: |||:||||:
Qy 275 LeuTyrThrGlnSerTyrGluAspProGluProAspMetGluValMetGluIleAsnPro 294
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3227 ATTTATCTGCCAAA----- 3241
Qy 295 LysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLeuAsnLeuValGln 314
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3242 -----GGAATATCGATTATGCTCTGCAATCACAGTC 3271
Qy 315 GlyAlaGlyGlnValValSer-----ValAspCysAsnProAlaGlnSerAla 330
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3272 TCCCGTCCGGAAGTGGTCAACGGCGATACGGACGTTATCTGCTCAACAGTATCCGCCAC 3331
Qy 331 LeuLeuGluLeuLysLysValAlaIleGlnLeuGluPheGluAspValTrpGlnLeu 350
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3332 ATTCTGGCTGTACGAAAGACTACACTGCTGCNAATCGAC----- 3370
Qy 351 PheGlyGluGlyValHisProArgIleGluLeuLeuTyrGluLysLysLeuAlaProPhe 370
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3371 -----ACACTTATCCGGCAACTGGCTGAA----- 3394
Qy 371 LeuSerGlnThrSerHisAsnPheTyrSerLysArgLeu-----TyrTyrPheGlnHis 388
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3395 ATCTCATCAATCACAGAAGATTATGGCGGTAAACCCGACCTGGAGCTGGGCCATGAACAG 3454
Qy 389 GlyLeuTyrTyrGlnGlyGlyMetGlyLysLeuCysTyrTrpValLeuGln----- 404
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3455 GAT-----TTTCGGCTGGT-----TGCTGGCTGACTGAGAAACCGGAACCC 3496
Qy 405 ---CysLeuAlaValValLeuGlyLeuGlyLysThrValLysArg----- 418
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3497 GCAATGAAAGCCATTATCCCGCAACCTTCAGCCGTGAATCTGCGCTGACCTGATGCAACGC 3556
Qy 419 -----LeuAlaAsnAlaProThrMetGluGluGlnArg----- 430
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3557 TCCGGGATGCTGTCAATTAATGATGCGCAGACCCCGTGATACATGTTACCGTCACTGGAG 3616
Qy 431 -----LeuTrpAspSerAsnMetLeuIleHisPhe----- 440
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3617 TACGNTAATTTCCGGAATCAGTGAAGAGATATTTCTGAGTACGTTTGAGCAGCTACAC 3676
Qy 441 -----ValLysAsnGlyProLysProLeuValTrp 450
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3677 CAGAAATAAGGATGAAGTGTGTTGAGCGAGAGTGATCAACCTCTTCAGAGGGTTGAGCTGG 3736
Qy 451 LeuPhe-----ValLysPheValSerLeuValLeuPheAsnLysAlaVal 465
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3737 AATTACAAAACCAATGCCCCCTGTAATTTGGCAATAAAATTTATCGTCAACAATCTGTGTG 3796
Qy 466 LeuTrpPheGlyGlyGly-----ValProGlyLysGlnTyrAlaLeuIleLysAla 482
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3797 AGGTGGGACCGGTGGGATGTCATCTTATCCCGGCAACAGGCAGATAGACTT---GCC 3853
Qy 483 Asp-----GlyIleProIle-----GluAsn 489
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3854 GACCTGGAAAGAAATGCTGCATCTGTTTCAGCGCAAAACCGATCCCGACACAGGGAAC 3913
Qy 490 TyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHisValArgLysGlnAsnTyr 509
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3914 ATAACATATTATCTGGACGAT-----CACATCCGCTCT----- 3946
Qy 510 PheTyrTyrAsnCysLeuThrGlyLysPheLeuArgAspAsn-----CysPro 525
      :|||:||||: |||:||||: |||:||||: |||:||||:

Db 3947 -----CTTCAGGAAAAGAAATGCTATGAAGATGAGATGCTCATTATTAAA 3991
Qy 526 ThrTyrLeuArgGluAlaAlaPheAlaThrLeu---LysSerGlyValValAspAsnLeu 544
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 3992 TACTTTAAGAGGGCTCTGGCCACATCACCGTTCAGGAAGCCAGAACTCGTTGACAGACTG 4051
Qy 545 ThrValSerThrAsnPheMetGluGluLeuLysAlaArgThrTyrThrLysValIle 564
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 4052 -----AATGATATTATCGCAAGACA----- 4072
Qy 565 LeuMetAspHisValAspTrpLeuAspMetProValAlaAsnGluLeuAlaGluCys--- 583
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 4073 CTATCTGACATGCTGGCAGTATAGCTTTGGCAGTATGCTCAAAGCTCGGAAATTTGTCGG 4132
Qy 584 -----LeuAlaLysGlnValAla-----ProGlyGlyIleVal 594
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 4133 ATAAGATATGATCGTGGGGCATATAACCGGTTTTCAGATGTCATACCGGTGGGCATACT- 4191
Qy 595 IleTrpArg 597
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 4192 GTCTGGAG 4200

RESULT 15
US-10-684-141-57
; Sequence 57, Application US/10684141
; Publication No. US20050003536A1
; GENERAL INFORMATION:
; APPLICANT: Furusawa, Mitsuru
; TITLE OF INVENTION: METHOD AND SYSTEM FOR RAPIDLY CONFERRING
; FILE REFERENCE: 690116.401
; CURRENT APPLICATION NUMBER: US/10/684,141
; CURRENT FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 7119
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-684-141-57

Alignment Scores:
Pred. No.: 0.0106 Length: 7119
Score: 123.00 Matches: 144
Percent Similarity: 33.7% Conservative: 83
Best Local Similarity: 21.4% Mismatches: 214
Query Match: 3.6% Indels: 234
DB: Gaps: 36

US-10-620-914-45 (1-648) x US-10-684-141-57 (1-7119)
Qy 107 HisSerLeuCysGluValAlaLysLysLysLysAlaLys---GlyTrpLysAsnVal 125
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 1307 CATAATCTC-----AAGCAGCTCCCAAGGCCAAACTTGGCTATGACCTGTGA 1354
Qy 126 GlnValValGluAlaAspAlaCysGlnPheAlaProGluGlyThrAlaThrLeuIle 145
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 1355 GAGCTGGACCTGAGGACATGTGCTATGCCC---ACTGAACAGCCCCAGACTGTGCC 1411
Qy 146 ThrPheSerTyrSer----- 150
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 1412 ACTTACTCAGTGTGAGTGTGCTACTTACTTACCTGTATGAAATAGCTCCACCCC 1471
Qy 150 ----- 150
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 1472 TTCATATTGCGCCTGTGTCACCATTTATCCCATGGAACCTGATGAGGTGCTCGGAAGGGC 1531
Qy 151 -----LeuThrMetIleProProPheHis---AsnValIle--- 161
      :|||:||||: |||:||||: |||:||||: |||:||||:
Db 1532 TCCGGGACACTGTGTGAAGCCCTTGTGATGTGTGCAAGCTTTCCATGCCAACATATCTTC 1591
Qy 162 -----AspGlnAlaCysSerTyrLeuSerGlnAspGlyLeuValGlyValAla 177
      :|||:||||: |||:||||: |||:||||: |||:||||:
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Db 1592 CCCAATAAGCAGCAGGAGTTCAACAAGCTGACAGATGATGCCACGTCGTAGATGCT 1651
Qy 178 AspPheTyrValSerGly-----LysTyrAspLeu 187
Db 1652 GAGACCTACGTTGGGGCCACCGTGGAGGCACTAGAGTCTGGTGTCTTCAGAAGTGTATC 1711
Qy 188 Pro-----LeuArgGlnMetProTrpSerArgPhePheTrpArgSerIlePheAsp 205
Db 1712 CCCTGCCGTTTAGGATGAATCCTCGACGCTTTCCTGCTGCAACGAGTCGAGAG 1771
Qy 206 IleAspAsnIleAspIleGlyProGluArgAlaTyrLeuGluGln-----LysLeu 223
Db 1772 ACTATGCCCCAGCCATTTGAAGAAGACAGAGGTGCTGTGGAAACAGCCACCACTTT 1831
Qy 224 GluArgValTrpGluGln-----AsnThrGlnGlySerIleProTyrValPro---Trp 240
Db 1832 CAAGAGGTGTGTGAGCAGATTAAAGACCAAGCTCACCTCCCTAAAGATGTTTCTTAACAGA 1891
Qy 241 LeuArgAlaPro-----TyrTyrValTrpIleGlyArgLeu---ProSerVal--- 255
Db 1892 ATTGAATGCTCTTAATCTATCATCTAGATGTGGGGCCATGTATCCTTAACATAATTCCT 1951
Qy 256 --GlyHisAlaLeuHisGluGluArgValGlu-ArgProProMetPheProProTrpPh 274
Db 1952 ACCAACCCCTACAGCCTTTCGCCATAGTGTGAGGCCACCTGTGCTGCTGTGACTTC 2011
Qy 274 eLeuTyrThrGlnSer-----TrpGluAspProGluProAspMetGluVa 289
Db 2012 AATAAGCCTGGAGCAAGTTGTGAGAGGAAGATGGCTGGC----- 2051
Qy 289 lMetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLe 309
Db 2052 -----AGTGGAGGGGAGAAATTC----- 2069
Qy 309 uAsnLeuLeuValGlnGlyAlaGlyGlnValValSerValAspCysAsnProAlaGlnSe 329
Db 2070 -----TGCCAGCCAGT-CGCAG 2085
Qy 329 rAlaLeuLeuGluLeuTysLysValAlaIleGlnGlnLeuGluPheGluAspValTrpGl 349
Db 2086 TGAATACCATCGGATTTCAG-----CATCAGCTGGAGTCGGAGAGTTTCCCCC 2133
Qy 349 nLeuPheGlyGluGlyValHisProArgIleGluGluLeu----- 362
Db 2134 TTTGTTTCCAGAGGGCCAGCACGGGCTTTTCCAGAGCTGTCCCGTGAAGAAGACGGCTAA 2193
Qy 363 -TyrGluLys--LysLeuAlaProPhe----- 370
Db 2194 ATATGAGAAGAGGAGCTGGCAGATTATTGCCGGAAGCCCTATAGAAAGATCCATGTGAC 2253
Qy 371 -----LeuSerGlnThrSerHisAsnPheTrpSerLysAr 382
Db 2254 CAAGGTAGAAGACGCTCTAACCCTACCTGCGAGGGGAAACTCAITTTATGTGGACAC 2313
Qy 382 gLeuTrpTyrPheGlnHisGlyLeuTyrTyrGlnGlyMetGlyLysLeuCysTrpVa 402
Db 2314 AGTGGGGCTTCAGAGACAGCGCGTATGAGTTCAAAGGACTGCACAAAGGTGTGGAAGAA 2373
Qy 402 lLeuGlnCysLeuAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAlaAsnAl 422
Db 2374 GAAGCTCTCGGCAGCTGTAGAGGTGGGGGATGCAATCAGAGGTGAAGCGCTGCAAGAAGC-- 2431
Qy 422 aProThrMetGluGluGlnArgArgLeuTrpAspSerAsnMetLeuIleHis----- 439
Db 2432 -----ATGGAGATCTTTTACGATTCACCTGCGAGCTGGCTCACAGTGCAT 2475
Qy 440 -----PheValLysAsnGlyProLysProLeuValTrpLeuPh 452
Db 2476 CCTGAACTCTTTCACGGCTATGTCATCGCAAGAGGAGCTCGC-----TGGTATTC 2526
Qy 452 eValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyVa 472
Db 2527 CATGGAGATGGCTGGTATCTGCTGCTTTACA-----GGAGCCAAACAT 2568
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Qy 472 lProGlyLysGlnTyrAlaLeuIleLysAlaAspGlyIleProfile----- 487
Db 2569 CATCACCCCAAGAGAGAACTGATTGAGCAGATCGGAGGCTTTAGAAATTTGGACACCGA 2628
Qy 488 -----GluAsnTyrIleAlaAArgThrMetAs 496
Db 2629 CGGAATATGGTGCCTCTACCCCAATAGCTTTCTCGTAAATTTTGTTCATCAAGACA----- 2683
Qy 496 pGlyValAlaGluAsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuTh 516
Db 2684 -----ACCAATGCGAAGAACCCAACTACCATCTCTCTATCTCTGCTGCTGCTT 2733
Qy 516 rGlyLysPheLeuArgAspAsnCysProThrTyr-----LeuArgGluAlaAl 532
Db 2734 GAACATCATGTCTCAAGGAAGGCTTTTCCAAACACCAAGTACCAGGAACCTAACAGAGCCTTC 2793
Qy 532 aPheAlaThrLeuLysSerGlyValValAspAsnLeuThrValSerThrAsnPhePheMe 552
Db 2794 GTCTCTCACCTAT-----GTCAACCCACTCTGAGAATAGTATCTT 2832
Qy 552 tGluGluLeuLysAlaAArgThrTyrThrLysValIleLeuMetAspHisValAspTrpLe 572
Db 2833 TTTTGAAGTCGATGGA---CCATACCTTGCTATGATCCTT----- 2869
Qy 572 uAspMetProValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGl 592
Db 2870 -----CCAGCTTCCCAAGGAAGCAAGAGCTGAAGAAAAGATATGCT----- 2914
Qy 592 yIleValIleTrpArgSerAlaSerLeuSerProProTyrAlaGluLeuIleGlnLysAl 612
Db 2915 ---GTGTTCAATGAAGATGTTCTCTTG-----GCTGAACGTG-----AA 2949
Qy 612 aGlyPheAspValArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgValAsnMe 632
Db 2950 AGGTTTTTGAGGTGAAA-----CGCCGAGGGGAGTTGCAGCTGATTAAAAAT 2994
Qy 632 tTyr---SerSerPheTyrMetAlaArgArgLysGlyAla 644
Db 2995 ATTCAGTCTCTCAGTCTTTTGGAGGCTTCTCTCAAGGGCAGC 3034
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Search completed: May 4, 2006, 18:08:56
Job time : 1427 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2006, 17:45:30 ; Search time 2237 Seconds
(without alignments)
1179.707 Million cell updates/sec

Title: US-10-620-914-45
Perfect score: 3463
Sequence: 1 MGSRGDPASYTKNFSLE.....RVNMYSSFYMARRKGAKDON 648

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB.spool/US10620914/runat 04052006 130319 18939/app query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -HOST=abs02h
-USER=US10620914 @CGN 1.1 660 @runat 04052006 130319 18939 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
1: /SID55/ptodata/2/pubpna/US08 NEW PUB.seq1.*
2: /SID55/ptodata/2/pubpna/US06 NEW PUB.seq1.*
3: /SID55/ptodata/2/pubpna/US07 NEW PUB.seq1.*
4: /SID55/ptodata/2/pubpna/US08 NEW PUB.seq1.*
5: /SID55/ptodata/2/pubpna/PT NEW PUB.seq1.*
6: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq1.*
7: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq1.*
8: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq2.*
9: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq1.*
10: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq1.*
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12: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq3.*
13: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq4.*
14: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq1.*
15: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq2.*
16: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq3.*
17: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq4.*
18: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq5.*
19: /SID55/ptodata/2/pubpna/US60 NEW PUB.seq1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	118.5	3.4	1155	17	US-11-234-786-373	Sequence 373, App
2	118.5	3.4	1155	18	US-11-139-041-301	Sequence 301, App
3	118.5	3.4	1185	18	US-11-139-041-335	Sequence 335, App
4	118.5	3.4	1590	18	US-11-139-041-323	Sequence 323, App
5	118.5	3.4	2000	17	US-11-234-786-374	Sequence 374, App
6	118.5	3.4	2000	18	US-11-139-041-302	Sequence 302, App
7	118.5	3.4	2040	17	US-11-234-786-375	Sequence 375, App
8	118.5	3.4	2040	18	US-11-139-041-303	Sequence 303, App
9	115.5	3.3	1155	18	US-11-139-041-328	Sequence 328, App
10	115.5	3.3	1512	17	US-11-234-786-368	Sequence 368, App
11	115.5	3.3	1512	18	US-11-139-041-294	Sequence 294, App
12	110	3.2	939	18	US-11-139-041-344	Sequence 344, App
13	109.5	3.2	1853	17	US-11-234-786-369	Sequence 369, App
14	109.5	3.2	1853	18	US-11-139-041-295	Sequence 295, App
15	107.5	3.1	876	18	US-11-139-041-341	Sequence 341, App
16	107.5	3.1	876	18	US-11-139-041-342	Sequence 342, App
17	107.5	3.1	879	17	US-11-234-786-531	Sequence 531, App
18	107.5	3.1	879	18	US-11-139-041-314	Sequence 314, App
19	107.5	3.1	933	18	US-11-139-041-343	Sequence 343, App
20	107.5	3.1	1852	17	US-11-234-786-530	Sequence 530, App
21	107.5	3.1	1852	18	US-11-139-041-313	Sequence 313, App
22	106	3.1	2055	18	US-11-079-463-2274	Sequence 2274, Ap
23	104	3.0	3006	11	US-10-932-182A-4215	Sequence 4215, Ap
24	104	3.0	3006	11	US-10-932-182A-4215	Sequence 4215, Ap
25	102	2.9	1857	11	US-10-932-182A-2428	Sequence 2428, Ap
26	102	2.9	1857	11	US-10-932-182A-2428	Sequence 2428, Ap
27	102	2.9	3042	17	US-11-124-367A-21	Sequence 21, Appl
28	101.5	2.9	2598	18	US-11-079-463-4664	Sequence 4664, Ap
29	101.5	2.9	7437	11	US-10-932-182A-1448	Sequence 1448, Ap
30	101.5	2.9	7437	11	US-10-932-182A-1448	Sequence 1448, Ap
31	101	2.9	2067	18	US-11-079-463-2719	Sequence 2719, Ap
32	101	2.9	3063	17	US-11-169-041-29	Sequence 29, Appl
33	99.5	2.9	2530	10	US-10-821-234-276	Sequence 276, App
34	99	2.9	2299	18	US-11-072-512-652	Sequence 652, App
35	99	2.9	1457619	17	US-11-098-686-8739	Sequence 8739, Ap
36	98	2.8	26214	11	US-10-330-773-222	Sequence 222, App
37	97.5	2.8	2315	18	US-11-072-512-1818	Sequence 1818, Ap
38	97	2.8	6942	14	US-11-301-554-1894	Sequence 1894, Ap
39	97	2.8	14279	18	US-11-224-663-191	Sequence 191, App
40	97	2.8	14279	18	US-11-224-525-191	Sequence 191, App
41	97	2.8	163162	17	US-11-121-086-66	Sequence 66, Appl
42	96.5	2.8	1851	17	US-11-234-786-366	Sequence 366, App
43	96.5	2.8	1851	18	US-11-139-041-291	Sequence 291, App
44	96.5	2.8	1851	18	US-11-139-041-292	Sequence 292, App
45	96.5	2.8	2184	17	US-11-234-786-370	Sequence 370, App

ALIGNMENTS

RESULT 1
US-11-234-786-373
; Sequence 373, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION

```
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-373

Alignment Scores:
Pred. No.: 0.134 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 17 Gaps: 11

US-10-620-914-45 (1-648) x US-11-234-786-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
204 CTTCCTCGTCTGCAGGGGAGTGGCAAGCAACGTGGCGCTTCTGGAGA----- 254
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 -----CCACGACGACTCTCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 GACACTCAGGAACAAGATGGGCAAGTGGTGTGCCACTGTCTCCCTCTCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluArg 263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 CGGCAAGAACGAAGTGGGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGAGCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 GTACCACTCCG-----TGGAAGAATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db GGACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCCAGAAAGATCTCATCGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GCTACGGGACACTGACGTGACACAGACGACGACAAAGAGGAGCTGCTTCATCTCGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValva 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 540 CTCTGCCAATGGGAATTCAGAAGTAGTAAAACTCTCTGCTGCACACGACGATGCACTTAA 599
Qy 320 lserValaspCysasnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleG1 340
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCTTTGAC---AACAAAAAGAGACAGCTCTGTATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG1 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
645 ATGCCAGGAGATGAATGTGGTTAATGTTCTGCGACATGGCAATATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisasnPheTrps 380
Db ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
705 AGATGAGTATGGAATACCACTCTGCACCTAGCTATCTATAATGAAGATAAAATTAATGCG 764
Qy 380 erLysArgLeuTrpTyr 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
765 CAAGACACTGCTCTTAT 781

RESULT 2
US-11-139-041-301
; Sequence 301, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419CJ5
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-301

Alignment Scores:
Pred. No.: 0.134 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-301 (1-1155)
```

```
QY 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
204 CTTCCCTCGTCGAGGGGAGTGGCAAGACGACGCTGGCGCTTCTGGAGA----- 254
QY 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 -----CCACGACGACTCTGCTAT-----GAA 275
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrrpLeuArgAlaPro 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 GACACTCAGGAACAAGATGGGCAAGTGGTGTGCTGCTCCCTGCTGAGGGGAG 335
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGACAGTGCCTTTCATGGAGCCAG 395
QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 GTACCAAGTCCG-----TGGAGAGATCT 419
QY 283 -----ProGluProAspMetGluValMe 290
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 GGACAAGCTCCACAGAGTGCCTGGTGGGTAAAGTCCCGCAGAAAGGATCTCATGTCAT 479
QY 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GCTCAGGACACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGTCGACAGACGATGCTCAACTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleGl 340
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCCTTGAC---AACAAAAAGAGGACAGCTCTGATAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
645 ATGCCAGGAAGATGAATGTGCGTTAATGTGCTGGAAACATGGCAGCTGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrps 380
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
705 AGATGAGTATGGAAATACCCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGCC 764

RESULT 3
US-11-139-041-335
; Sequence 335, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
```

```
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-335

Alignment Scores:
Pred. No.: 0.138 Length: 1185
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-335 (1-1185)
QY 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
204 CTTCCCTCGTCGAGGGGAGTGGCAAGACGACGCTGGCGCTTCTGGAGA----- 254
QY 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 -----CCACGACGACTCTGCTAT-----GAA 275
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrrpLeuArgAlaPro 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 GACACTCAGGAACAAGATGGGCAAGTGGTGTGCTGCTCCCTGCTGAGGGGAG 335
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGACAGTGCCTTTCATGGAGCCAG 395
QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 GTACCAAGTCCG-----TGGAGAGATCT 419
QY 283 -----ProGluProAspMetGluValMe 290
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
420 GGACAAGCTCCACAGAGTGCCTGGTGGGTAAAGTCCCGCAGAAAGGATCTCATGTCAT 479
QY 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
480 GCTCAGGACACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGTCGACAGACGATGCTCAACTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleGl 340
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
600 TGTCCTTGAC---AACAAAAAGAGGACAGCTCTGATAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
645 ATGCCAGGAAGATGAATGTGCGTTAATGTGCTGGAAACATGGCAGCTGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrps 380
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
705 AGATGAGTATGGAAATACCCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGCC 764
```

```
Qy 380 erLysArgLeuTrpTyr 385
Db 765 CAAGACACTGCTCTTAT 781

RESULT 4
US-11-139-041-323
; Sequence 323, Application US/111139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hiest, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-323

Alignment Scores:
Pred. No.: 0.199 Length: 1590
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-323 (1-1590)
Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgPhePheTrpArgSerIlePhe 204
Db 639 CTTCCCTGCTGCGAGGGGGAGTGGCAAGACAGCGTGGCGCTTCTGGAGA----- 689
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 690 -----CCACGACGACTCTCTAT-----GAA 710
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 711 GACACTCAGGAACAAGATGGGCAAGTGTGTGCTGCACGTCTCCCTCTGCAGGGGGAG 770
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluArg 263
```

```
Db 771 CGCAAGAGCAAGCTGGGGCGCTTGGGGAGACTACGATGACAGYGCCTTCATGGAGCCAG 830
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 831 GTACCAGTCCG-----TGAGAAGATCT 854
Qy 283 -----ProGluProAspMetGluValMe 290
Db 855 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAGGATCTCATCGTCTAT 914
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 915 GCTCAGGGACACTGACGTGACACAGAGGACACAAAGAGGACTGCTCTACATCTGGC 974
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlnGlyAlaGlyGlnValva 320
Db 975 CTCCTGCAATGGGAATTTCAGAAAGTAGTAAAACTCTGCTGGACACAGCATGCTCAACTTAA 1034
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGl 340
Db 1035 TGTCTTGTAC---AACAAAAAGAGGACAGCTCTGTATAAG-----GCCGTACA 1079
Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 1080 ATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACATGCACTGATCCAAATATTCC 1139
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnHeTrpS 380
Db 1140 AGATCAGTATGGAATACCACTCTGCACCTATCTATTAATGAAGATAAATTAATGGC 1199
Qy 380 erLysArgLeuTrpTyr 385
Db 1200 CAAAGCACTGCTCTTAT 1216

RESULT 5
US-11-234-786-374
; Sequence 374, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; TITLE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
```

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Db      765 CAAGCACTGCTCTTAT 781

RESULT 6
US-11-139-041-302
; Sequence 302, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Devin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-302

Alignment Scores:
Pred. No.: 0.265 Length: 2000
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-302 (1-2000)

Qy      187 LeuProLeuArgGlnMetProTrp-----SerArgPhePheTrpArgSerIlePhe 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      204 CTTCCCTGCTGCGAGGGGGAGTGCAAGAGCAAGTGGCGCTCTCGAGA----- 254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      255 -----CCACGACGACTCTGCTAT-----GAA 275

Qy      225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      276 GACACTCAGGACCAAGATGGCGAGTGGTGTGCACTGCTTCCCTGTCGAGGGGAG 335
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      336 CGGCAAGACAAAGTGGCGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCCG 395
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

US-11-139-041-303
; Sequence 303, Application US//11139041
; Publication NO. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US//1139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-303

Alignment Scores:
Pred. No.:          0, 272           Length:      2040
Score:             118.50         Matches:       66
Percent Similarity: 37.4%        Conservative: 19
Best Local Similarity: 29.1%     Mismatches:   81
Query Match:       3.4%         Indels:       61
DB:                18          Gaps:         11

US-10-620-914-45 (1-648) x US-11-139-041-303 (1-2040)
QY    187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
      |||||...|||
Db    204 CTTCCCTCGTCTGCAGGGGGAGTGCCAAGACAGTCGGCGCTTCGGAGA----- 254

QY    205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrlLeuGluGlnLysLeuGlu 224
      |||||...|||
Db    255 -----CCACGACGACTCTGCATAT-----GAA 275

QY    225 ArgValTrpGluGlnAsnThrGlnClySerIleProTyrValProTrpLeuArgAlaPro 244
      |||||...|||
Db    276 GACACTCAGGAACAAGATGGGCAAGTGTGTGCTGCTTCCCCTGCTGCAGGGGGAG 335

QY    245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
      |||||...|||
Db    336 CGGCAAGACCAAGTGGCGCTTGGGGAGACTACGATGACAGTCGCTTCATGGAGCCAG 395

QY    264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
      |||||...|||
Db    396 GTACCACGCTCG-----TCGAGAGATCT 419

```

```
Alignment Scores:
Pred. No.: 0.268 Length: 1155
Score: 115.50 Matches: 65
Percent Similarity: 37.4% Conservatives: 20
Best Local Similarity: 28.6% Mismatches: 81
Query Match: 3.3% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-328 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
|||
Db 204 CTTCCCTGCTGCAGGGGAGTGGCAAGAGCAACGTGGCGCTCTCGAGA-----254

Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
|||
Db 255 -----CCAGGAGCTCTGCTAT-----GAA 275

Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
|||
Db 276 GACACTCAGGACACAGATGGGCAAGTGTGTGCCACTGCTCCCTGCTCAGGGGAG 335

Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
|||
Db 336 CAGCAAGAGCAAGGTGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGAGCCCGAG 395

Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
|||
Db 396 GTACCACGTCCG-----TGAGAGAAGATCT 419

Qy 283 -----ProGluProAspMetGluValMe 290
|||
Db 420 GGACAGCTCCACAGAGCTGCTGTTGGGTAAAGTCCCAGAAAGATCTCATCGTCAT 479

Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
|||
Db 480 GCTCAGGGACACTGACGTGAACAAGCAGCAGCAAGCAAAAGAGGACTGCTCTACATCTGGC 539

Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
|||
Db 540 CTCGCCAATGGGAATTGAGAGTAGTAAATCTCTGCTGGACAGACGATGTCACACTAA 599

Qy 320 LserValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleGl 340
|||
Db 600 TGTCTTGAC--AACAAAAAGAGCAGACTCTGATAAG-----GCCGTACA 644

Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
|||
Db 645 ATGCCAGGAAGATGAATGTCGTTAAATGTTGCTGGACATGGCACTGATCCAAATATTCC 704

Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
|||
Db 705 AGATGAGTATGGAAATACCACTCTGCACCTACGCTATCTATAATGAAGATAAATTAATGGC 764

Qy 380 erLysArgLeuTrpTyr 385
|||
Db 765 CAAGCACTGCTCTTAT 781

RESULT 10
US-11-234-786-368
; Sequence 368, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
```

```
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ailun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE OF INVENTION: POLYPEPTIDES THEREOF
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-368

Alignment Scores:
Pred. No.: 0.374 Length: 1512
Score: 115.50 Matches: 65
Percent Similarity: 36.6% Conservatives: 18
Best Local Similarity: 28.6% Mismatches: 83
Query Match: 3.3% Indels: 61
DB: 17 Gaps: 11

US-10-620-914-45 (1-648) x US-11-234-786-368 (1-1512)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
|||
Db 426 CTTCCCTGCTGCAGGGGAGTGGCAAGAGCAACGTGGCGCTCTCGAGA-----476

Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
|||
Db 477 -----CCAGGAGATCTGCTAT-----GAA 497

Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
|||
Db 498 GACACTCAGGAACAAGATGGCAAGTGTGTGCCACTGCTTCCCTGCTCAGGGGAG 557

Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
|||
Db 558 CRGCAAGAGCAAGGTGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGAGCCCGAG 617

Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
|||
Db 618 GTACCACGTCCG-----TGAGAGAAGATCT 641

Qy 283 -----ProGluProAspMetGluValMe 290
|||
```

Db 642 GGACAGCTCCACAGAGCTGCTGGTAAAGTCCCGAAGAGGATCTCATCTCAT 701
QY 290 t-----GluLeuAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 702 GCTCAGGAGACACTGACGTGAACAGAGACAAAGCAAGCAAGAGGAGCTGCTTACATCTGC 761
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 762 CTCTCCCAATGGGAATTCAGAAAGTAGTAAACTGTGCTGGGACAGACGATGTCAACTTAA 821
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleG1 340
Db 822 TGTCTCTTGAC---AACAAAAGAGACAGCTCTGAYAAAG-----GCCGTACA 866
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG1 360
Db 867 ATGCCAGGAAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGATCCAAATATTCC 926
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
Db 927 AGATGAGTATGGAATACACTTCTRCACCTAYGCTRTCTAYAAATGAAGATAAAATTAATGGC 986
QY 380 erLysArgLeuTrpTyr 385
Db 987 CAAGCACTGCTCTTAT 1003

RESULT 11

US-11-139-041-294
; Sequence 294, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-294

Alignment Scores:

Pred. No.: 0.374 Length: 1512

Score: 115.50 Matches: 65
Percent Similarity: 36.6% Conservative: 18
Best local Similarity: 28.6% Mismatches: 83
Query Match: 3.3% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-294 (1-1512)

QY 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db 426 CTTCCTCTGCTGCAGGGGAGTGGCAAGCAAGCAAGCTGGCGCTTCTGGAGA-----476
QY 205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 477 -----CCACGACGAYTCTGCTAT-----GAA 497
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 498 GACACTCAGGAACAGATGGGCAAGTGGTGTGCCACTGTCTCCCTGCTGCAGGGGAG 557
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 558 CRGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATCACAGTGCCTTCATGGAGCCAG 617
QY 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 618 GTACCACGTCGG-----TGGAAGAGATCT 641
QY 283 -----ProGluProAspMetGluValMe 290
Db 642 GGACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGGATCTCATCTCAT 701
QY 290 t-----GluLeuAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 702 GCTCAGGAGACACTGACGTGAACAGAGGACAAAGCAAGAGGAGTGTCTTACATCTGC 761
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 762 CTCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGACAGACGATGTCAACTTAA 821
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysValAlaIleG1 340
Db 822 TGTCTCTTGAC---AACAAAAGAGACAGCTCTGAYAAAG-----GCCGTACA 866
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGlyGlyValHisProArgIleG1 360
Db 867 ATGCCAGGAAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGATCCAAATATTCC 926
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
Db 927 AGATGAGTATGGAATACACTTCTRCACCTAYGCTRTCTAYAAATGAAGATAAAATTAATGGC 986
QY 380 erLysArgLeuTrpTyr 385
Db 987 CAAGCACTGCTCTTAT 1003

RESULT 12

US-11-139-041-344
; Sequence 344, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137

```
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-344

Alignment Scores:
Pred. No.: 0.738 Length: 939
Score: 110.00 Matches: 63
Percent Similarity: 36.3% Conservative: 22
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 3.2% Indels: 64
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-344 (1-939)
Qy 183 GlyIystrAspLeuProLeuArgGlnMetProTrpSerArg- 197
Db 72 GGGCAAGTGTGCTGCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGCAACGTGGG 131
Qy 198 PhehetrPArgSerIlePheaspIleaspIleaspIleGlyProGluArgAla 217
Db 132 CACTCTCGAGA- 158
Qy 218 TyrLeuGluGlnLysLeuGluArgValTrpGluGlnAsnThrGlnGlySerIleProTyr 237
Db 159 -----TGTGAAGACGCTTGGGAGCAAGAGTCCAAAGTGTGCTGCCACTG 203
Qy 238 ValProTrpLeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerValGly--- 256
Db 204 CTTCCCTGCTGCAGGGGAGCGGCAAGAGCAACGTGCTTGGGAGACTACGATGA 263
Qy 257 HisAlaLeuHisGluGluArgValGluArgProProMetPheProThrPheLeuTyr 276
Db 264 CAGCGCCCTTCATGGATCCAGGTACCACTCCA- 296
Qy 277 ThrGlnSerTrp-GluAsp- 283
Db 297 -----TGGAGAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGTAAAGTCCC 347
Qy 283 oGluProAspMetGluValMet-----GluIleAsnProLysAsp----- 296
Db 348 CAGAAAGGATCTCATCGTCATGCTCAGGAGACAGGATGTGAACAAGAGGACAAAGAAA 407
Qy 297 ----ThrValLeuThrLeuThrSer-----GlyGlyCysAsnAlaLeuAsnLeuVal 313
Db 408 GAGGACTGCTTACATCTGGCTTGGCTTCGCCAATGGGAATTCAGAAGTAGTAAACTCGTCT 467
Qy 313 lGlnGlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAlaLeuGln 333
Db 468 GGACAGAGATGTCACTTAATGTCTTGAC----AACAAAGAGGACAGCTCTGACAA 524
```

```
Qy 333 uLeuLysLysValAlaIleGlnLeuGluPheGluaspValTrpGlnLeuPheGlyG1 353
Db 525 G-----GCCGTACAATCCAGGAAGATGTCGCTTAATGTTGCTGGAAACA 572
Qy 353 uGlyValHisProArgIleGluGluLeuTyr-GluLysLysLeuAlaProPheLeuSerG 373
Db 573 TGGCACTGATCCAATATTCAGATGAGTATGGAAATACCACTCTACACTATGCTGCTA 632
Qy 373 lnThrSerHisAsnPheTrpSerLysArgLeuTrpTyr 385
Db 633 CAATGAAGATAAATAATGGCCAAAGCACTGCTCTTAT 670
```

```
RESULT 13
US-11-234-786-369
; Sequence 369, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-369

Alignment Scores:
Pred. No.: 1.92 Length: 1853
Score: 109.50 Matches: 64
Percent Similarity: 36.1% Conservative: 18
Best Local Similarity: 28.2% Mismatches: 84
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Query Match:	3.2%	Indels:	61
DB:	17	Gaps:	11
US-10-620-914-45 (1-648) x US-11-234-786-369 (1-1853)			
Qy	187	LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe	204
Db	426	CTTCCCTCTCTCAGGGGAGTGGCAAGACAACTGGGCGCTTCTGGAGA-----	476
Qy	205	AspIleAsnIleAspIleGlyProGluArgArgAlaTrpLeuGluGlnLysLeuGlu	224
Db	477	-----CCACGACGAYTCTGCTAT-----GAA	497
Qy	225	ArgValTrpGluGlnAsnThrGlnGlySerIleProTrpValProTrpLeuArgAlaPro	244
Db	498	GACACTCAGAAACAAGATGGGCAAGTGTGTGCTCCTTCCCTGTCTGCAGGGGGAG	557
Qy	245	TyrTyrValTrpIleGlyArgLeuProSerValGly--HisAlaLeuHisGluGluArg	263
Db	558	CRGCAAGACAAAGTGGGCGCTTGGGGAGACTACGATGACAGYGCCTTCATGGAKCCGAG	617
Qy	264	ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp--	282
Db	618	GTACCACGCTCC-----TGACAGAGATCT	641
Qy	283	-----ProGluProAspMetGluValMe	290
Db	642	GGCAAGCTCCACAGAGCTGCCTGGTGGGTAAAGTCCCCAGAAAGGATCTCATGCTCAT	701
Qy	290	t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh	302
Db	702	GCTCAGGGACACKAYGTGAACAGARGGACAAAGAGGAGTCTCTACATCTGGC	761
Qy	302	rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyValGlnValVa	320
Db	762	CTCTGCCAATGGGAATTCAGAGTAGTAAACTCTGCTGGACAGCAGTGTCACTTAA	821
Qy	320	lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleG	340
Db	822	TGTCCTTGAC--AACAAAGAGGACAGCTCTGAYAAAG-----GCCGTACA	866
Qy	340	nglnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG	360
Db	867	ATGCCAGGAATGAATGCTGGCTTAATGTTCTGGAACTGGCCTGATCCAAATATTC	926
Qy	360	uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS	380
Db	927	AGATGAGTATGGAATACACTCTRCACTAYGCTRTCTTAAATGAAGATAAATAATGCG	986
Qy	380	erLysArgLeuTrpTyr	385
Db	987	CAAGCACTGCTCTTAT	1003
RESULT 14			
US-11-139-041-295			
; Sequence 295, Application US/11139041			
; Publication No. US20060083749A1			
; GENERAL INFORMATION:			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Hirst, Shannon Kathleen			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Foy, Teresa M.			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Persing, David H.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.419C15			
; CURRENT APPLICATION NUMBER: US/11/139,041			
; PRIOR FILING DATE: 2005-05-25			
; PRIOR APPLICATION NUMBER: US 10/079,137			
; PRIOR FILING DATE: 2002-02-20			
; PRIOR APPLICATION NUMBER: US 09/924,400			
; PRIOR FILING DATE: 2001-08-07			

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; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-295

Alignment Scores:
Pred. No.: 1.92 Length: 1853
Score: 109.50 Matches: 64
Percent Similarity: 36.1% Conservative: 18
Best Local Similarity: 28.2% Mismatches: 84
Query Match: 3.2% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-295 (1-1853)
QY 187 LeuProLeuArgGlnMetProTTP-----SerArgArgPhePheTTPArgSerIlePhe 204
Db 426 CTTCCCTCGCTGCAGGGGGAGTGGCAAGAGCAACGTGGCGCTTCTGGAGA----- 476
QY 205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 477 -----CCAGCAGCATCTCGTAT-----GAA 497
QY 225 ArgValTTPGluGlnAsnThrGlnGlySerIleProTyrValProTTPLeuArgAlaPro 244
Db 498 GACACTCAGGAACAAGATGGTGGCAAGTGTGTGCTGCTTCCCTGCTGCAGGGGGAG 557
QY 245 TyrTyrValTTPIleGlyArgLeuProSerValGly--HisAlaLeuHisGluGluArg 263
Db 558 CRGCAAGAGCAAGGTGGCGCGCTTGGGGAGACTACGATGACAGYGCCTTCATGGAKCCGAG 617
QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTTP-GluAsp-- 282
Db 618 GTACCACGTCCR-----TGAGAAATCT 641
QY 283 -----ProGluProAspMetGluValMe 290
Db 642 GGACAAGCTCCACAGAGCTGCCTGGTGGGTAAAGTCCCAGAAAGGATCTCATCTGCAT 701
QY 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 702 GCTCAGGGACACKGAYGTGAACAAGARGGACACAGCAAAAGAGGACTGCTCTACATCTGGC 761
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValVa 320
Db 762 CTTCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGCTGGACAGACGATGTCACTTAA 821
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGl 340
Db 822 TGTCTCTGCAC--RACAAAAAGAGCAGCTCTGAYAAAG-----CCCGTACA 866
QY 340 nGlnLeuGluPheGluAspValTTPGlnLeuPheGlyGluGlyValHisProArgIleGl 360

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RESULT 14
US-11-139-041-295
; Sequence 295, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF BREAST CANCER
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07

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